

16.rup

32	320.5	19.9	343	1	GP81_MOUSE	O8c131 mus musculu
33	320.5	19.9	361	1	P2Y4_RAT	O35811 rattus norv
34	319	19.8	328	1	P2Y6_RAT	O63371 rattus norv
35	319	19.8	373	1	P2Y2_MOUSE	P35383 mus musculu
36	318	19.7	362	1	P2YR_CHICK	P34996 gallus gall
37	318	19.7	362	1	P2YR_MELGA	P49652 meleagris g
38	318	19.7	374	2	O57466	O57466 meleagris g
39	317.5	19.7	346	1	CLT2_HUMAN	O9nb75 homo sapien
40	317	19.6	309	1	CLT2_RAT	O324t9 rattus norv
41	315.5	19.5	361	1	P2Y4_MOUSE	Q9jj87 mus musculu
42	315.5	19.5	365	1	P2Y4_HUMAN	P51582 homo sapien
43	315.5	19.5	396	1	BRB2_RAT	P25023 rattus norv
44	312.5	19.4	364	2	Q68DM6	Q68dm8 homo sapien
45	312.5	19.4	391	1	BRB2_HUMAN	P30411 homo sapien

## ALIGNMENTS

RESULT 1  
GP35\_HUMAN  
ID GP35\_HUMAN STANDARD; PRT; 309 AA.  
AC Q9HC97; O43495; Q86UH4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Probable G protein-coupled receptor GPR35.  
GN Name=GPR35; (Human)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;  
RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,  
RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;  
RT "Discovery of three novel G-protein-coupled receptor genes.";  
RL Genomics 47:310-313(1998)  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;  
RX MET-253 AND SER-294.  
RA MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,  
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
RA Bell G.I.;  
RT "Genetic variation in the gene encoding calpain-10 is associated with  
RT type 2 diabetes mellitus";  
RL Nat. Genet. 26:163-175(2000).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT SER-294.  
RA Warren C.N., Aronstam R.S., Sharma S.V.;  
RT "CDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues  
CC examined, including pancreatic islets and skeletal muscle, with  
CC relatively higher levels in adult lung, small intestine, colon and  
CC stomach.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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28	87.8	9.4	2582	3	US-08-944-496-6	Sequence 6, Appli
29	87.8	9.4	2582	3	US-08-925-767-6	Sequence 6, Appli
30	87.4	9.4	1077	4	US-09-170-496D-39	Sequence 39, Appli
31	87.4	9.4	1077	4	US-09-170-496D-185	Sequence 185, App
32	86	9.2	1113	4	US-09-826-509-540	Sequence 540, App
33	86	9.2	1805	3	US-08-405-271A-18	Sequence 18, Appl
34	86	9.2	1373	4	US-09-016-434-1391	Sequence 1391, Ap
35	86	9.2	1373	4	US-09-023-655-1417	Sequence 1417, Ap
36	86	9.2	3205	4	US-09-976-594-171	Sequence 171, App
37	85.6	9.2	2025	4	US-09-016-434-1482	Sequence 1482, Ap
38	85.6	9.2	2025	4	US-09-814-915A-74	Sequence 74, Appl
39	82.4	8.9	1842	1	US-08-442-134A-1	Sequence 1, Appli
40	82.4	8.9	1842	1	US-08-444-581B-1	Sequence 1, Appli
41	82.4	8.9	1842	1	US-08-446-088A-1	Sequence 1, Appli
42	81	8.7	1594	2	US-08-955-713-1	Sequence 1, Appli
43	80.6	8.7	1059	3	US-09-576-160B-9	Sequence 9, Appli
44	79	8.5	1059	3	US-09-576-160B-8	Sequence 8, Appli
45	79	8.5	1285	4	US-09-016-434-1366	Sequence 1366, Ap

## ALIGNMENTS

RESULT 1  
US-09-422-869-21  
; Sequence 21, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOKISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG I.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Human  
US-09-422-869-21

Query Match	99.0%	Score 920.4	DB 3	Length 1875
Best Local Similarity	99.4%	Pred. No. 6.5e-197		
Matches 924	Conservative 0	Mismatches 6	Indels 0	Gaps 0
QY	1	ATGATGGCACCCTACAAACACCTGTGGCTCCAGCGACTCACCTGGCCCCCAGCGATCAAG	60	
Db	576	ATGATGGCACCCTACAAACACCTGTGGCTCCAGCGACTCACCTGGCCCCCAGCGATCAAG	635	
QY	61	CTGGGCTTCTACGCCCTACTTGGCGCTCTGTGGTGTAGGCTGTCTCAACAGCCTG	120	
Db	636	CTGGGCTTCTACGCCCTACTTGGCGCTCTGTGGTGTAGGCTGTCTCAACAGCCTG	695	
QY	121	GGGCTCTGGGTGTTCTGCTGGCGCATGCGAGTGGAGCGGACCGCGATCTACATGACC	180	
Db	696	GGGCTCTGGGTGTTCTGCTGGCGCATGCGAGTGGAGCGGACCGCGATCTACATGACC	755	
QY	181	AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGCCTTGTGTGTGACTCCCTG	240	
Db	756	AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGCCTTGTGTGTGACTCCCTG	815	
QY	241	CGAGACACCTCAGACACGCGGCTGTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG	300	

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RESULT 3  
US-09-724-864-29

US-09-422-869-1 Application US/09422869 : Sequence 1

; GENERAL INFORMATION:

APPLICANT: HORIKAWA, YUKIO  
APPLICANT: ODA NAOTICA

APPLICANT: SREENAN, SEAMUS

APPLICANT: OTANI, KENICHI

APPLICANT: BELL, GARENTE 1.  
: TITLE OF INVENTION: METHODS OF TREE

; CURRENT APPLICATION NUMBER: US/09/

;; EARLIER APPLICATION NUMBER: 60/134  
: EARLIER BILLING DATE: 1999-05-13

; SOFTWARE: PatentIn Ver. 2.0

LENGTH: 49136  
TYPE: DNA

RECEIVED: 1964

9

1

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28	308.5	19.1	375	4	US-09-947-922-3	Sequence 3, Appli
29	306	19.0	328	3	US-08-513-974B-39	Sequence 39, Appl
30	306	19.0	328	3	US-08-513-974B-371	Sequence 371, App
31	306	19.0	328	4	US-09-461-436B-39	Sequence 39, Appl
32	305.5	18.9	354	4	US-09-364-425B-60	Sequence 60, Appl
33	305.5	18.9	358	3	US-09-041-545-2	Sequence 2, Appli
34	305.5	18.9	358	3	US-09-327-925-2	Sequence 2, Appli
35	305.5	18.9	362	4	US-09-170-496D-4	Sequence 4, Appli
36	305	18.9	259	3	US-09-261-599B-3	Sequence 3, Appli
37	305	18.9	259	4	US-09-456-455A-3	Sequence 61, Appl
38	304.5	18.9	93	3	US-09-724-864-61	Sequence 186, App
39	304.5	18.9	358	4	US-09-170-496D-186	Sequence 2, Appli
40	304	18.8	342	4	US-09-054-272-2	Sequence 555, App
41	304	18.8	342	4	US-09-826-509-555	Sequence 39, Appl
42	303	18.8	326	1	US-08-118-270-39	Sequence 39, Appl
43	303	18.8	326	5	PCT-US93-08528-39	Sequence 4, Appli
44	302.5	18.7	373	2	US-08-559-524A-4	Sequence 4, Appli
45	302.5	18.7	373	3	US-08-749-707-4	Sequence 4, Appli

## ALIGNMENTS

## RESULT 1

US-09-422-869-20  
 ; Sequence 20, Application US/09422869  
 ; Patent No. 6235481

## GENERAL INFORMATION:

; APPLICANT: POLONSKY, KENNETH S.  
 ; APPLICANT: HORIKAWA, YUKIO  
 ; APPLICANT: ODA, NAOHISA  
 ; APPLICANT: COX, NANCY J.  
 ; APPLICANT: SREENAN, SEAMUS.  
 ; APPLICANT: ZHOU, YUN-PING  
 ; APPLICANT: OTANI, KENICHI  
 ; APPLICANT: HANIS, CRAIG L.  
 ; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/422,869

; CURRENT FILING DATE: 1999-10-21

; EARLIER APPLICATION NUMBER: 60/134,175

; EARLIER FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 20

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Human

US-09-422-869-20

## Query Match

Best Local Similarity 100.0%; Score 1614; DB 3; Length 309;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNGTYNTCGSSDLTWPPAIKLGFIAYLGVLVLLGLLNSLALWVFCRCMQWTETRIYNT	60
Db	1	MNGTYNTCGSSDLTWPPAIKLGFIAYLGVLVLLGLLNSLALWVFCRCMQWTETRIYNT	60
QY	61	NLAVADLCLLCTLPFLVLSRLDTSPTLCQLSQGIYLTNRNYSISLVTALAVDRVAVRH	120
Db	61	NLAVADLCLLCTLPFLVLSRLDTSPTLCQLSQGIYLTNRNYSISLVTALAVDRVAVRH	120
QY	121	PLRARGLSRQRAAACAVALWVLVIGSLVAVRWLIGIQGGFCFRSTRNFMSPPLLGF	180
Db	121	PLRARGLSRQRAAACAVALWVLVIGSLVAVRWLIGIQGGFCFRSTRNFMSPPLLGF	180
QY	181	YLPLAVVVFCSLKVVYTAQAQRPPTDVGQAEATRAARWVANLLVFVVCFLPHVGLTVR	240
Db	181	YLPLAVVVFCSLKVVYTAQAQRPPTDVGQAEATRAARWVANLLVFVVCFLPHVGLTVR	240
QY	241	LAUCWACALLETTRRALYITSKLSDANCLLDACIYTYMAKEFQASALAVAPRAKAHS	300

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Db 241 LAVGNACALLETIRRALYITSKLSDANCCDAICYYMAKEFOEASALAVAPRAKAHS 300  
QY 301 QDSLCVTLA 309  
Db 301 QDSLCVTLA 309

RESULT 2  
US-08-781-250-2  
; Sequence 2, Application US/08781250  
; Patent No. 6010877  
; GENERAL INFORMATION:  
; APPLICANT: Sathe, Ganesh  
; APPLICANT: Van Horn, Stephanie  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Mao, Joyce Yue  
; TITLE OF INVENTION: CDNA CLONE HB8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,250  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han,  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATGS0043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4060  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-250-2

Query Match 24.9%; Score 402; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 1.3e-26;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYVGLLVGLLNSLALWFCRMOQWETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81  
Db 44 AYVSVFLLGLIINSVSLFVFCRMRKSRSTAFITNLAVSDLLFVCTLPFKIPYFNH 103  
QY 82 -DTSDFPLCQSGIVLTNRYSISLVTAIADRYVAVRHPLRARGLSRQAAAVCAVL 140  
Db 104 WPGDIT-LCKISGTAFTLNIYGSMLFTICSDRFLAIVVPSRTIRTRNSAIVCAGV 162  
QY 141 WLVLGSLVARLLGQEG-----GGCFSTRHFNFSMR--FPLLGFLPLAVVVF 189  
Db 163 WILVLSGGISASLFTNNVNNATTCPEGFSKRWKTYLSKITFIEVWGFIIPLINVS 222  
QY 190 CSLKVVVTAQAQRPPTDVGQAEAT-RKAARMVWNLAVFVVCFLPHVGLTVRLAVGNAC 248  
Db 223 CSSVVLRLT--RKPATLSQIGTKNKKVLRMTVHMAVFFVVCFFPYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYMAKEFOEASALAVAPRAKAHSQDSIC 305  
Db 281 TNCFLERPAKIWPITLCLATLNCDFDFIYFTLESQKSFYI-----NAHIRMESLIF 334  
QY 306 VT 307  
Db 335 KT 336

RESULT 3  
US-09-170-496D-108  
; Sequence 108, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-108

Query Match 22.8%; Score 368.5; DB 4; Length 387;  
Best Local Similarity 34.3%; Pred. No. 9.6e-24;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLLVGLLNSLALWFCRMOQWETRIYMTNLAVADLCCLCTLPVL-----HSLR 81  
Db 34 LGLEFIPLGLLGLALWIFCPHLKSWKSRIFLFLNLAVADFLIILCLPVMYVYVRSOW 93  
QY 82 DTSDFPLCQSGIVLTNRYSISLVTAIADRYVAVRHPLRARGLSRQAAAVCAVL 141  
Db 94 NFGDIP-CRLVLFMFAMNRQSGIIFLTVAVDYFRVVPHPHALNKISNWTAAIISCLLW 152  
QY 142 VLIVIG---SLVARLLGQEG--GFCFR-STHNF--NSMRPFLGFLYPLAVVVFCSLK 193  
Db 153 GITVGLTVHLLKKLL-LQNGPANVCISFSICHTFRWHEMF-LLEFLPLGLIILFCSAR 210  
QY 194 VVTAQAQRPPTDVGQAEATRKARMMWNLAVFVVCFLPHVGLTVRLAVGW-----N 246  
Db 211 IIVSLRQR---QMDRHAKIKRAITIMVVAIVVICFLP---SVVVRIRIFLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCDAICYYMAKEP 283  
Db 265 NCEVYSVDLAPFITLSFTYMSMLDPVVVYFSPSF 301

RESULT 4  
US-09-170-496D-222  
; Sequence 222, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 387

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:17:30 ; Search time 19.5 Seconds  
(without alignments)  
1182.901 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTCCSSDLTPWPAIK.....AVAPRAKAHKSQDSLCTVLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A-COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCITUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614	100.0	309	3 US-09-422-869-20	Sequence 20, Appl
2	402	24.9	370	3 US-08-781-250-2	Sequence 2, Appl
3	368.5	22.8	387	4 US-09-170-496D-108	Sequence 108, App
4	368.5	22.8	387	4 US-09-170-496D-222	Sequence 222, App
5	368.5	22.8	387	4 US-09-944-807-21	Sequence 21, Appl
6	361.5	22.4	344	2 US-08-467-948A-8	Sequence 8, Appl
7	361.5	22.4	344	2 US-08-467-947A-8	Sequence 8, Appl
8	360.5	22.3	302	2 US-08-467-948A-30	Sequence 30, Appl
9	360.5	22.3	302	3 US-08-467-947A-30	Sequence 30, Appl
10	330.5	20.5	377	4 US-09-745-842-17	Sequence 17, Appl
11	329.5	20.4	374	4 US-09-102-710B-3	Sequence 3, Appl
12	321	19.9	362	3 US-08-513-974B-374	Sequence 374, App
13	319.5	19.8	346	4 US-09-585-876-2	Sequence 2, Appl
14	318	19.7	374	4 US-09-745-842-15	Sequence 15, Appl
15	317	19.6	373	3 US-08-513-974B-373	Sequence 373, App
16	315.5	19.5	365	4 US-09-745-842-16	Sequence 16, Appl
17	315.5	19.5	365	4 US-09-077-173D-2	Sequence 2, Appl
18	312.5	19.4	364	4 US-08-148-708-2	Sequence 2, Appl
19	311.5	19.3	391	4 US-09-826-509-463	Sequence 463, App
20	310.5	19.2	327	3 US-08-513-974B-372	Sequence 372, App
21	310.5	19.2	362	4 US-09-170-496D-166	Sequence 166, App
22	310	19.2	342	3 US-08-988-876-9	Sequence 9, Appl
23	308.5	19.1	375	1 US-08-442-134A-2	Sequence 2, Appl
24	308.5	19.1	375	1 US-08-444-581B-2	Sequence 2, Appl
25	308.5	19.1	375	1 US-08-446-088A-2	Sequence 2, Appl
26	308.5	19.1	375	1 US-08-559-524A-3	Sequence 3, Appl
27	308.5	19.1	375	3 US-08-749-707-3	Sequence 3, Appl

28	308.5	19.1	375	4 US-09-947-922-3	Sequence 3, Appl
29	306	19.0	328	3 US-08-513-974B-39	Sequence 39, Appl
30	306	19.0	328	3 US-08-513-974B-371	Sequence 371, App
31	306	19.0	328	4 US-09-461-436B-39	Sequence 39, Appl
32	305.5	18.9	354	4 US-09-364-425B-60	Sequence 60, Appl
33	305.5	18.9	358	3 US-09-041-545-2	Sequence 2, Appl
34	305.5	18.9	358	3 US-09-327-925-2	Sequence 2, Appl
35	305.5	18.9	362	4 US-09-170-496D-4	Sequence 4, Appl
36	305	18.9	259	3 US-09-261-599B-3	Sequence 3, Appl
37	305	18.9	259	4 US-09-456-455A-3	Sequence 3, Appl
38	304.5	18.9	93	3 US-09-724-864-61	Sequence 61, Appl
39	304.5	18.9	358	4 US-09-170-496D-186	Sequence 186, App
40	304	18.8	342	4 US-09-054-272-2	Sequence 2, Appl
41	304	18.8	342	4 US-09-826-509-555	Sequence 555, App
42	303	18.8	326	1 US-08-118-270-39	Sequence 39, Appl
43	303	18.8	326	5 PCT-US93-08528-39	Sequence 39, Appl
44	302.5	18.7	373	2 US-08-559-524A-4	Sequence 4, Appl
45	302.5	18.7	373	3 US-08-749-707-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-422-869-20  
; Sequence 20, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-422-869-20

Query Match	100.0%;	Score 1614;	DB 3;	Length 309;
Best Local Similarity	100.0%;	Pred. No. 7.1e-130;	Mismatches 0;	Indels 0;
Matches 309;	Conservative 0;			Gaps 0;
QY	1	MNGYNTCCSSDLTPWPAIKLGFAYLVLLVGLLLSLALWFCRCRQQTETRIYMT	60	
Db	1	MNGYNTCCSSDLTPWPAIKLGFAYLVLLVGLLLSLALWFCRCRQQTETRIYMT	60	
QY	61	NLAVADICLCTLPFVLSLRTSDTCLCOLSQGLYLTNRYSISLVTAIADRVYVVRH	120	
Db	61	NLAVADICLCTLPFVLSLRTSDTCLCOLSQGLYLTNRYSISLVTAIADRVYVVRH	120	
QY	121	PLRAGRLSPROAAACAVLWLVIGSLVARLLQEGGFCFRSTRHNFNSMRFPPLG	180	
Db	121	PLRAGRLSPROAAACAVLWLVIGSLVARLLQEGGFCFRSTRHNFNSMRFPPLG	180	
QY	181	YLPLAVVFCSLKVVTALAQRPPTDVQAEATKAAARMVWVNLVFCFLPHVGLTVR	240	
Db	181	YLPLAVVFCSLKVVTALAQRPPTDVQAEATKAAARMVWVNLVFCFLPHVGLTVR	240	
QY	241	LAHGWNACALLETIRALYITSKLSDANCLDAICYYWYMAKEFOEASALAVAPRAK	300	
Db	241	LAHGWNACALLETIRALYITSKLSDANCLDAICYYWYMAKEFOEASALAVAPRAK	300	

Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYVYMAKEFQBSALAVAPRAKAHKS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309  
RESULT 2  
US-08-781-250-2  
; Sequence 2, Application US/08781250  
; Patent No. 6010877  
; GENERAL INFORMATION:  
; APPLICANT: Sathe, Ganesh  
; APPLICANT: Van Horn, Stephanie  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Mao, Joyce Yue  
; TITLE OF INVENTION: CDNA CLONE HB8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,250  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han,  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG50043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4060  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-250-2  
Query Match 24.9%; Score 402; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 1.3e-26;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;  
QY 25 AYLGVLVLLGLLNSLALWVFCRCMQWTETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81  
Db 44 AVYSVVFILGLIITSVSLFVFCFRMKWRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
QY 82 -DTSVTPQLCSQGIYLTNRYMSISLVTAIVDQYVAVRHPLRARGLRSPROAAVCAVL 140  
Db 104 WPGDPT-LCKISGTAFTNIGSMFLTCTISVDRFLAIVYFPRSTRITRRNSAIVCAGV 162  
QY 141 WLVLGSLVARWLLGQEG-----GGFCFRSTRHNFSMR--FPLLGFLYPLAVVVF 189  
Db 163 WLVLGGGSLASLFTSTNNNATTCFEGFSKRWKLYLSKIITFIEVVGFIPLINVS 222  
QY 190 CSLKVVYTAQAQRPPTDVQAEAT--RKAARMVMWANLLVVFVVCFLPHVGLTVRLAVGNAC 248  
Db 223 CSSVVLRLT--RKPAATLSQIGTNKKVKLXMITVHMAVVFVVCFLPVYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDAICYVYMAKEFQBSALAVAPRAKAHKSQDSLC 305  
Db 281 TNCFLERFAKIMPIITLCLATLNCDFPIFYFTUESFKSPYI-----NAHIRMESLF 334  
QY 306 VT 307  
Db 335 KT 336  
RESULT 3  
US-09-170-496D-108  
; Sequence 108, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-108  
Query Match 22.8%; Score 368.5; DB 4; Length 387;  
Best Local Similarity 34.3%; Pred. No. 9.6e-24;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;  
QY 27 LGVLLVLGLLNSLALWVFCRCMQWTETRIYMTNLAVADICLLCTLPFVL-----HSLR 81  
Db 34 LGLEFIFGLLGNLALWIFCFHLKSKSRIFLPLNLAVADFLIICLPVMDYVYVRRSDM 93  
QY 82 DTSVTPQLCSQGIYLTNRYMSISLVTAIVDQYVAVRHPLRARGLRSPROAAVCAVL 141  
Db 94 NFGDIP-CRLVLFMFPMNRQSGIIFLTIVVAVDRYFVRVHPHNLKINSWTAAIISCLLW 152  
QY 142 VLIVG--SLVARWLLGQEG--GFCFR-STRHNR--NSMRPPLGFLYPLAVVVFCSLK 193  
Db 153 GITVGLTVHLLKKKLL-IQNGPANCISFSICHTFRWHEAMF-LLEFLPLGLIILFCSAR 210  
QY 194 VVTAQAQRPPTDVQAEATRKAARMVMWANLLVVFVVCFLPHVGLTVRLAVGN-----N 246  
Db 211 IISLRLQ---QMDRHAKIKRAITIMVVAIVVICFLP---SVVVRIRIFWLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCLDAICYVYMAKEF 283  
Db 265 NCEVRSVDLAPFITLSFTYNSMLDPVVVYFSPSF 301

RESULT 4  
US-09-170-496D-222  
; Sequence 222, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 387

Query Match	22.4%;	Score 361.5;	DB 2;	Length 344;
Best Local Similarity	29.2%;	Pred. No. 3.4e-23;		
Matches	90;	Conservative 68;	Mismatches 107;	Indels 43; Gaps 10;
QY	10	SSDLTWPPAIIKLGFAYL-GVLLVLGLLNSIALVFCRCRQOQWTFRIYMTNLAVADLC	68	
DB	6	SSHCFFNDSFKTYLGCMSFWMLLIGLISNCVAIYIFICVLKVRNRTTYMINLMSDLL	65	
QY	69	LLCTLFPVLHSLRDTSDTP- ---LCOLSQIGVLTNRNYSISLTAIADVRYAVRHLPLRA	124	
DB	66	FVFTLPFRIFYF-TTENWFPGLDLCKISVMLFYTNMYGSIILFTLCISVDFLAIVYPFKS	124	
QY	125	RGURSPQAAACAVLWLVLI-GSLVARMLLQIEGG- ---FCFRSTRHNFNSMRPP- -	176	
DB	125	KTLTTRKRNKIVCTGVMLTVIGGSAPAVFQSTHSGQNSASEACFN- ---FPEA	175	
QY	177	-----LLGFYFLPLAVVVFCSLKVVYALAAQRPPTDVGOAEATR-KAARWVWA	221	
DB	176	TKWTYLSRIVIFIEIVGFFPIPLILNVTCSMWLKLTK- ---PVLTSRSKINKTKVLKMFV	233	
QY	222	NLLAVFVVCFLPHVGHGTVRLAVGWNNA- ---CALLETIRRALYITPSKLDANCCLDATCYYY	278	

Db 234 HLIIFCFVFPYNILYSLVRTQTFCVNCVAAVRTWYPITLCAVSNCCFDPVYVF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301

## RESULT 7

US-08-467-947A-8  
; Sequence 8, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-947A-8

Query Match 22.4%; Score 361.5; DB 3; Length 344;  
Best Local Similarity 29.2%; Pred. No. 3.4e-23;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIIKLGFIAYL-GVLLVLGLLLNSIALWVFCRCMQOWTETRIYMTNLAVADLC 68  
Db 6 SHCFFYNDSPKTYLGCMSFVGLISNCVAIYIFICVLKVRNFTTMYMINLAMSDDL 65  
QY 69 LLCTLPFVLHSLRDTSDTP----LCOLSQGIYLTNRYSISLVTATADVRYAVRHLPLRA 124  
Db 66 FVFTLPRFIFYF-TTRNWFPGDLLCKISWMLFTNMYGSLIFLTCISVDRFLAIVYVFKS 124  
QY 125 RGLRSQRQAACAVILWLVLI-GSLVARMILGTOEGG-----FCFSTRHNFNSMRFPP-- 176  
Db 125 KTLKTRKNAKIVCTGVMLTVIGGSAPAVFVQSTHSQGNNAACFPEN-----FPEA 175

QY 177 -----LLGFYLPVAVVFGSLKVVTTALAQRPPTDVGQABATR-KAARMVMA 221  
Db 176 TKWYLSRIVFIEIVGFPIPLINVTCTSSMWLKLTK--PVTLSRSKINKTKVKMIFV 233  
QY 222 NLLVFWCFLPHVGLTVRLAVGNA---CALLETIRRALYITTSKLSDANCCLDICYY 278  
Db 234 HLIIFCFVFPYNILYSLVRTQTFCVNCVAAVRTWYPITLCAVSNCCFDPVYVF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301

## RESULT 8

US-08-467-948A-30  
; Sequence 30, Application US/08467948A  
; Patent No. 5998164  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR2  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,948A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-467-948A-30

Query Match 22.3%; Score 360.5; DB 2; Length 302;  
Best Local Similarity 30.0%; Pred. No. 3.6e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIIKLGFI-AYLGVLLVLGLLLNSIALWVFCRCMQOWTETRIYMTNLAVADLC 68  
Db 1 SENCSTEDSFKTYLGCVFMSFVGLIANCVAIYIFTTLKVRNFTTMYMLAISDLL 60  
QY 69 LLCTLPFVLHSLRDTSDTP----LCOLSQGIYLTNRYSISLVTATADVRYAVRHLPLRA 124

Db 61 FVETLPPFRYYF-VVRNWPFGDVLCKISVTLFVTNNMYGSLFLTCISVDRFLAIVHPFRS 119  
 QY 125 RGLSPROAAACAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----FP- 176  
 Db 120 KTLRTKRNARIVCVAVIITVLGASTPASF-----FQSTNRQNTTEQRTCFENFPE 169  
 QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVQQAETRAKAAWVA 221  
 Db 170 STWKTVLSRVIVFIEIVGFFIPLILNVCTSTWVLR1L-NKPLTSLRNKLSKKKVLKMFV 228  
 QY 222 NLLVFWVFCPLPHVGL---TVRLAVGNWACALLETIRRALYITSKLSDANCCLDALCYYY 278  
 Db 229 HLIVFCFCFVPYNITLILYSLMRTQTWNCVSVTVAVRTPVTLCAVNSCCFDPVIVYF 288

## RESULT 9

US-08-467-947A-30  
 ; Sequence 30, Application US/08467947A  
 ; Patent No. 6090575

## GENERAL INFORMATION:

; APPLICANT: LI, YI  
 ; APPLICANT: CAO, LIANG  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: GENTZ, REINER  
 ; APPLICANT: BULT, CAROL J.  
 ; APPLICANT: SUTTON III, GRANGER G.  
 ; APPLICANT: ROSEN, CRAIG A.  
 ; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
 ; TITLE OF INVENTION: Coupled Receptor GPR1  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 ; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 ; CITY: WASHINGTON

; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK  
 ; COMPUTER: IBM PC COMPATIBLE  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/467,947A  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/04079

; FILING DATE: 30-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 302 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-08-467-947A-30

Query Match 22.3%; Score 360.5; DB 3; Length 302;  
 Best Local Similarity 30.0%; Pred. No. 3.6e-23;  
 Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;

QY 10 SSDLTWPPAKLGFY-AYLGVLLVGLLNSLALWVFCRCMQQWTTETRIYMTNLAVADLC 68

Db 1 SSNCSTEDSFKTYLGCVFMSVFLGLIANCAVAIYFTLTKVRNETTMYMLLAISDL 60

## RESULT 11

US-09-102-710B-3

; Sequence 3, Application US/09102710B

; Patent No. 6479630

QY 69 LLCTLPFVLHSLURDSDTP-----LCQLSQGIYLTNRYMSISLVTAIAVDYRVAVRHPLRA 124  
 Db 61 FVETLPPFRYYF-VVRNWPFGDVLCKISVTLFVTNNMYGSLFLTCISVDRFLAIVHPFRS 119  
 QY 125 RGLSPROAAACAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----FP- 176  
 Db 120 KTLRTKRNARIVCVAVIITVLGASTPASF-----FQSTNRQNTTEQRTCFENFPE 169  
 QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVQQAETRAKAAWVA 221  
 Db 170 STWKTVLSRVIVFIEIVGFFIPLILNVCTSTWVLR1L-NKPLTSLRNKLSKKKVLKMFV 228  
 QY 222 NLLVFWVFCPLPHVGL---TVRLAVGNWACALLETIRRALYITSKLSDANCCLDALCYYY 278  
 Db 229 HLIVFCFCFVPYNITLILYSLMRTQTWNCVSVTVAVRTPVTLCAVNSCCFDPVIVYF 288

## RESULT 10

US-09-745-842-17

; Sequence 17, Application US/09745842

; Patent No. 6762029

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollloper, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.

; TITLE OF INVENTION: P2Y12 Receptor

; FILE REFERENCE: 44481-5053-US

; CURRENT APPLICATION NUMBER: US/09/745,842

; CURRENT FILING DATE: 2000-12-26

; PRIOR APPLICATION NUMBER: US 60/171,622

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur

US-09-745-842-17

Query Match 20.5%; Score 330.5; DB 4; Length 377;

Best Local Similarity 33.1%; Pred. No. 1.6e-20;

Matches 90; Conservative 47; Mismatches 108; Indels 27; Gaps 8;

QY 28 GVLLVGLLNSLALWVFCRCMQQWTTETRIYMTNLAVADLCCLLCTLPFVLHSLURDSDTP 87

Db 41 GVVCVGLCLNAVALYIFLCRLKTNASTTYMFHLAVSDALYASLPLLVYTYARGDHP 100

QY 88 ---LCQLSQGIYLTNRYMSISLVTAIAVDYRVAVRHPLRARGLSPROAAACAVLWVL 143

Db 101 FSTVLCKLVRFLFTNLVCSILFLTCISVHRCLGLRPLRLSRWGRARYARVAGAVVWL 160

QY 144 VIG--SLVARWLLG1QEGGFCFRSTRN-----FNSMRFPPLGLFYLPLAVVVF 189

Db 161 VLACQAPVLYFVTTTSARGG--RVTCHTSAPELSRFRVAYSSVLMGLL-FAVPPAVILV 216

QY 190 CSLKVVTALAQRP--TDVGQAETRAKAAWMAWVWVWVFCFLPHVGLTVRLAVGW-- 245

Db 217 CVVLMARLL-KPAYGTSGGLPRAKRSVRTIAVLAVALFALCFLPFHVTRTLVYSPRSLD 275

QY 246 NCALLETIRRALYITSKLSDANCCLDALCY 277

Db 276 LSCHTLAINMAYKVTRFLASANSCLDPVLYF 307

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: RN09402
; US-09-102-710B-3

Query Match          20.4%; Score 329.5; DB 4; Length 374;
Best Local Similarity 29.2%; Pred. No. 1.9e-20;
Matches 99; Conservative 54; Mismatches 121; Indels 59; Gaps 10;

QY      2 NGTYNTCGSSDLTWPPAIKGF-----YAYL-----GVLVGLLLSLALWVFCCR 48
DB      9 NSTINGTWEGD-----ELGYKCFNEDFKYVLLPVSYGVCVGLCLNVAIYFLCR 61

QY      49 MQOWTEIRYMTNLAVADLCILCTLPFVLHSLRDTSDTP----LCOLSQGIYLTRNYSI 104
DB      62 LKTWNASTTYMHLVASDSLYAASLEPLIVYYAQGDHPFFSTVICKLVRFIFYNLVCSI 121

QY      105 SLVTALADVRYAVRHPLRARGLRSPROAAACAVLWLVIQS-----LVARWLLGIQE 158
DB      122 LFETCSIVRSGLVRPLHLSRWGHARVARVAAVVWVLVLAQTVPVLYFTTSVGT-- 179

QY      159 GGCFPRSTRHN-----FNMRPPLLGFLYPLVAVVFCSLKVVTALAQRPTDV 206
DB      180 -----RITCHDTSDELPSHFVAYSVMGLGLL-FAVPFSIIICVCMARELLKPAYGTT 233

QY      207 GQAEATRKARWMWANLLFYVVCFLPHVGLTVRLAVGW--NACALLEITIRALIYISKL 264
DB      234 GLPRAKRKSVRTIALVLAVALCFLPFHVTRTLVYSFRSLDISCHTLNAINMAYKITRPL 293

QY      265 SDANCCLDIAICYV-----MAKEFOEASALAVAPRAK 296
DB      294 ASANSCLDPVLIPLAGQRLRVFARDAKPAKTEPTSPQAR 332

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryco
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukushima, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:31:16 ; Search time 204 Seconds  
(without alignments)  
7459.497 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
Sequence: 1 atgaatggcactcaaacac.....tgctgagcctcgctctaa 930

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	920.4	99.0	1875	US-09-422-869-21	Sequence 21, Appli
2	920.4	99.0	49136	US-09-422-869-1	Sequence 1, Appli
3	141.8	15.2	1854	US-09-724-864-29	Sequence 29, Appli
4	111.6	12.0	1098	US-09-170-496D-225	Sequence 225, App
5	111.2	12.0	1089	US-09-170-496D-3	Sequence 3, Appli
6	111.2	12.0	1365	US-09-016-434-1429	Sequence 1429, Ap
7	110	11.8	1098	US-09-170-496D-117	Sequence 117, App
8	110	11.8	1597	US-08-724-974A-1	Sequence 1, Appli
9	110	11.8	1697	US-09-364-425B-26	Sequence 26, Appli
10	109.6	11.8	1089	US-09-170-496D-165	Sequence 165, App
11	92.6	10.0	1128	US-09-170-496D-193	Sequence 193, App
12	91	9.8	1128	US-09-170-496D-201	Sequence 201, App
13	91	9.8	1815	US-09-041-545-1	Sequence 1, Appli
14	91	9.8	1815	US-09-327-925-1	Sequence 1, Appli
15	89	9.6	1167	US-09-826-509-574	Sequence 574, App
16	89	9.6	1317	US-09-016-434-1446	Sequence 1446, Ap
17	87.8	9.4	1128	US-09-711-889-1	Sequence 1, Appli
18	87.8	9.4	1128	US-09-170-068-1	Sequence 1, Appli
19	87.8	9.4	1128	US-09-170-496D-55	Sequence 55, Appli
20	87.8	9.4	1128	US-09-170-496D-69	Sequence 69, Appli
21	87.8	9.4	2582	US-08-480-994-6	Sequence 6, Appli
22	87.8	9.4	2582	US-08-1616-844-6	Sequence 6, Appli
23	87.8	9.4	2582	US-08-599-654-6	Sequence 6, Appli
24	87.8	9.4	2582	US-08-485-573-6	Sequence 6, Appli
25	87.8	9.4	2582	US-08-944-868A-6	Sequence 6, Appli
26	87.8	9.4	2582	US-08-944-423A-6	Sequence 6, Appli
27	87.8	9.4	2582	US-08-925-743-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-422-869-21  
; Sequence 21, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SEENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Human  
US-09-422-869-21

Query Match 99.0%; Score 920.4; DB 3; Length 1875;  
Best Local Similarity 99.4%; Pred. No. 6.5e-197;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGAATGGCACCCTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 60  
Db 576 ATGAATGGCACCCTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 635  
QY 61 CTGGGCTTCTAGCCCTACTTGGGCGTCTGTGGTGTAGGCTGCTGCTCAACGCTTG 120  
Db 636 CTGGGCTTCTAGCCCTACTTGGGCGTCTGTGGTGTAGGCTGCTGCTCAACGCTTG 695  
QY 121 GCGCTCTGGGTGTTCTGCTGCGCATGAGAGTGGAGCGACCGCATCTACATGACC 180  
Db 696 GCGCTCTGGGTGTTCTGCTGCGCATGAGAGTGGAGCGACCGCATCTACATGACC 755  
QY 181 AACCTGGGGTGGCGGACCTCTGCTGCTGTGTCACCTTTGCCCTTGTGCTGCACTCCCTG 240  
Db 756 AACCTGGGGTGGCGGACCTCTGCTGCTGTGTCACCTTTGCCCTTGTGCTGCACTCCCTG 815  
QY 241 CGAGACACTCAGACACCGCGCTGTGCGAGCTCTCCGAGGCGATCTACTTACACACAG 300



```

; Sequence 29, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Murison, James D.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Mouse
US-09-724-864-29

Query Match          15.2%; Score 141.8; DB 3; Length 1854;
Best Local Similarity 71.5%; Pred. No. 1.6e-22;
Matches 201; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

Qy 549 GCATGTCGTGGGCCAACCTCTCGTGTGTTGTCGTCTCTGCCCCCTGCAGCTGGG 708
Db 4 CACATGTCGTGGGCCAACCTTGGCTGTGTTTGTATCTGCTTCTCGCCCTTGCATGGTGC 63

Qy 709 CTGACAGTCGCCTCGCAGTGGGCTGGAACGCCCTGTGCCCTCTCTGGAGAGCATCCGTCGC 768
Db 64 CTGACCGTGCAGGTCTCCCTGAACCTCAATACCTGTGCTGCCCGAGACACTTCAGCCGT 123

Qy 769 GCCCTGTACATAACAGCAAGCTCTCAGATGCCAACTGTGCTCTGGAGCGCATCTGCTAC 828
Db 124 GCCCTGTCCATCACAGGTAAACTCTCAGACACCAACTGTGCTCTGGATGCCATCTGTTAC 183

Qy 829 TACTACATGCGCAAGAGATTCCAGGAGCGGTCTGCACTGGCGGTGGCTCCCCGTGCTAAG 888
Db 184 TACTACATGCGCAGAGAGTTCCAGGAAGCGTCCAAAGCAGCCAGCTTTCC---AACACA 240

Qy 889 GCCCAAAAGCCAGGACTCTCTGTGCGTGACCCCTCGCCTA 929
Db 241 CCCCAAGAGCCAAAGATTCCCAGATCCTGAGCCTCACCTA 281

RESULT 4
US-09-170-496D-225
; Sequence 225, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339--Endogenous, Constitutively Activated Human G Protein
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-225

Query Match          12.0%; Score 111.6; DB 4; Length 1098;
Best Local Similarity 50.4%; Pred. No. 8.2e-16;
Matches 403; Conservative 0; Mismatches 364; Indels 33; Gaps 4;

Qy 87 CTTGCTGGTGCTAGGCTGTGCTCAACAGCGTGGCGCTCTGGGTGTCTTGCTGCCGCAT 146
Db 90 CGTCTGGTGGTGGCTTCCGGGCAACTGCTGTCCCTCTACTTCCGCTACCTGCAGAT 149

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US-09-170-496D-3

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Query Match      12.0%; Score 111.2; DB 4; Length 1089;
Best Local Similarity 50.3%; Pred. No. 1e-15;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 98 TAGGCTGTCTCAACAGCCTGGGGCTCTGGGTGTTCTGTCGCGCATGACAGAGTGA 157
Db 89 TGGGGTGGCCCAACCACTGCTGCTCTGTGGGGCGCTACCGCCAGGTGCAACAGCA 148

QY 158 CGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGACCTCTGCGCTGTGACCT 217
Db 149 ACGAGTGGCGCTTACCTGATGAACCTCAGCATCGCCGACCTGTGTACATCTGACGC 208

QY 218 TGCCCTTCTGTGCTGACTCCCTGCGAGAC-----ACCTCAGACACCGCTGT 265
Db 209 TGCCGCTGTGGTGGACTTCTCTGACCAACAGCAACTGGATCAACGGCCCGGTCT 268

QY 266 GCAGCTCTCCAGGCGATCTACCTGACCAACAGGTATACATGAGCATCAGCCTGGTCA 325
Db 269 GCAAGCTCTTGGGTTCATCTTACACCAATATCTACATCAGCATCGCTTCTGTGCT 328

QY 326 CCATCGCGTGAACCGCTATGTGGCGGTGGCGACCGCTGCGTGCCTGGCGGTGCGGT 385
Db 329 GCATCTCGGTGACCGCTACCTGGCTGTGGCCACCACTCCGCTTGGCCGCTGCGCC 388

QY 386 CCCCAGGACAGCTGGCGCGGTGGCGGTCTCTGGGTGCTGTGTCATCGGCTCCCTGG 445
Db 389 GCGTCAAGACCGCGGTGGCGGTGAGCTCGGTGCTGGGCCACGAGCTGGCGCCAACT 448

QY 446 TGCGCTGTCTCTGGGGATTCAGAGGGCGGTCTCTGCTTTCAGGAGCACCCGCGACA 505
Db 449 CGCGGCCCTGTTCATGACGAGCTCTCCGAGACCGCTAGAACACACCTTCTGCTTTG 508

QY 506 ATTTCAACTCCATGCGGTTCGCGTCTGGGATTCATCTGCGCCCTGGCGGTGGTCT 565
Db 509 AGAAGTTCCTCCATGGAAGCTGGGTGGCTGGATGAACCTCTATCGGTGTTCTGGGT 568

QY 566 TCTGCTCCCTGAAGTGTGACTGCGCTGGCCGAGAGGCCACCCAGAGCTGGGCGAGG 625
Db 569 TCCCTCTTCCTGGCGCTCATGCTGCTGTAACCGGGGATCTCTGCGGCGCTGCGGG 628

QY 626 CAGAGGCCACCGCAGGCTAAAGCATGCTTGGGCCAACTCTCTGGTGTTCGTGCTCT 685
Db 629 GCAGCGTGTCCACGAGCCCGAGGAGGCCAAGATCAAGCGGTGGCCCTCAGCCTCA 688

QY 686 GTTCTCTGCCCTG 699
Db 689 TCGCCATCGTGTG 702
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RESULT 6

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US-09-016-434-1429
; Sequence 1429, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1429:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9598152
; US-09-016-434-1429

Query Match      12.0%; Score 111.2; DB 4; Length 1365;
Best Local Similarity 50.3%; Pred. No. 1.1e-15;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 98 TAGGCTGTCTCAACAGCCTGGGGCTCTGGGTGTTCTGTCGCGCATGACAGAGTGA 157
Db 305 TGGGGTGGCCCAACCACTGCTGCTGTGGGGCGCTACCGCCAGGTGCAACAGCA 364

QY 158 CGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGACCTCTGCGCTGTGACCT 217
Db 365 ACGAGTGGCGCTTACCTGATGAACCTCAGCATCGCGACCTGTGTATCATCTGACGC 424

QY 218 TGCCCTTCTGTGCTGACTCCCTGCGAGAC-----ACCTCAGACACCGCTGT 265
Db 425 TGCCCTTCTGTGCTGACTTCTCTGACCAACAGCAACTGGATCAACGGCCCGGTCT 484

QY 266 GCAGCTCTCCAGGCGATCTACCTGACCAACAGGTATACATGAGCATCAGCCTGGTCA 325
Db 485 GCAAGCTCTTGGGTTCATCTTACACCAATATCTACATCAGCATCGCTTCTGTGCT 544

QY 326 CCATCGCGTGAACCGCTATGTGGCGGTGGCGACCGCTGCGTGCCTGGCGGTGCGGT 385
Db 545 GCATCTCGGTGACCGCTACCTGGCTGTGGCCACCACTCCGCTTGGCCGCTGCGGC 604

QY 386 CCCCAGGACAGCTGGCGCGGTGGCGGTCTCTGGGTGCTGTGTCATCGGCTCCCTGG 445
Db 605 GCGTCAAGACCGCGGTGGCGGTGAGCTCGGTGCTGGGCCACGAGCTGGGCGCCAACT 664

QY 446 TGCGCTGTCTCTGGGGATTCAGGAGGGCGGTCTCTGCTTTCAGGAGCACCCGCGACA 505
Db 665 CGCGCCCTCTTCCATGACGAGCTCTTCCGAGACCGCTAGAACACACACCTTCTGCTTTG 724

QY 506 ATTTCAACTCCATGCGGTTCGCGTCTGGGATTCATCTGCGCCCTGGCGGTGGTGTCT 565
Db 725 AGAAGTTCCTCCATGGAAGCTGGGTGGCTGGATGAACCTCTATCGGTGTTCTGGGT 784

QY 566 TCTGCTCCCTGAAGTGTGACTGCGCTGGCCGAGAGGCCACCCAGAGCTGGGCGAGG 825
Db 785 TCTCTTCCCGTGGCGCTCATGCTGCTGTCTGCGGGGATCTCTGCGGCGGTGCGGG 844

QY 626 CAGAGGCCACCGCAGGCTAAAGCATGCTTGGGCCAACTCTCTGGTGTTCGTGCTCT 685
Db 845 GCAGCGTGTCCACGAGCCCGAGGAGGCCAAGATCAAGCGGTGGCCCTCAGCCTCA 904

QY 686 GTTCTCTGCCCTG 699
Db 905 TCGCCATCGTGTG 918
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RESULT 7  
US-09-170-496D-117  
; Sequence 117, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 117  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-170-496D-117

Query Match 11.8%; Score 110; DB 4; Length 1098;  
Best Local Similarity 50.2%; Pred. No. 1.9e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
QY 87 CCTGCTGTGTAGGCTGCTCTCAACAGCGCTGGCGTCTGGGTGTTCTGTCGCCGAT 146  
DB 90 CGTGTGTGTGGGCTTCCCGGCAACTGCTGTCCTCTACTTCCGCTACCTGAGAT 149  
QY 147 GCAGAGTGGACGAGACCGCATCTACATGACCACTGGGGTGGCGGACCTTGCT 206  
DB 150 CAAGGCCCGACGAGCTGGGCGTGTACCTGTGCAACCTGACGGTGGCGGACCTTCTA 209  
QY 207 GCTGTGACCTTGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266  
DB 210 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 269  
QY 267 CCAGCTCTCCAGGGCATCTACTGACC-----AACAGGTACATGAGCATCAG 314  
DB 270 CGACTGTCTCCAGGTGTGGGATCTCTCTGTACGAGACATCTACATCAGGTGG 329  
QY 315 CTGTGTACGGCCATCGCGTGGACCGTATGTGCGCGTGGCGGACCGCTGCGTGGCGG 374  
DB 330 CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 389  
QY 375 CGGGCTGGGTCCCCAGGAGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425  
DB 390 CCAGTTCGGGACCTTGAAGGGCGCGCTGGCGTTCAGCGTGGTCTCTGGGCCAAGAGCT 449  
QY 426 GCTGTGCTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485  
DB 450 GCTGACGAGCATCTACTTCTCTATGACGAGAGGTATCGAGGAGGAGAACAGCACCG 509  
QY 486 TTTCAGGAGCACCGGCAAAATTTCAACTTCATGCGGTTCCCGTCTGCTGCTGCTGCT 545  
DB 510 CGTGTGCTTTGAGCACTACCCCATCCAGGCATGGCAGCGCCCATCAACTACTACGCTT 569  
QY 546 GCCCTTGGCGTGGTGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605  
DB 570 CTTGTGGGCTTCTCTTCTCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629  
QY 606 ACC-----ACCGAGTGGGCGGACGAGGCGCCACCGAGGCTTAACGATGCT 656  
DB 630 CGCGCTGGCGGAGCGGCGGACCCAGAGAGCGCGAGGACAGATCCAGCGGCTGCT 689  
QY 657 CTGGGCGCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716  
DB 690 GCTCAGCACCGGTGCTCATCTTCTGCGCTGCTTCTGCGCTTCTGCGCTTCTGCTGCT 749  
QY 717 GGGCTCGAGTGGGCTGGAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776

DB 750 GCGAGC---GTCCTGGAGCGCAGCTGCGACTTCCCAAGGGGTTTTCACGCGCTACCA 806  
QY 777 CATAACAGCAAGCTTTCAGATGCAACTGTGCTGCGGACCATCTGCTACTACTACAT 836  
DB 807 CTTCTCCCTCTGCTCACCAGCTTCAACTGGCTGCGGACCCCGCTGCTCTACTGCTCGT 866  
QY 837 GGCCAAGAGTTCCAGGAGG 856  
DB 867 CAGCGAGACCCACCGGG 886

RESULT 8  
US-08-724-974A-1  
; Sequence 1, Application US/08724974A  
; Patent No. 5912335  
; GENERAL INFORMATION:  
; APPLICANT: Derk J. Bergsma, Catherine E. Ellis  
; TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor  
; TITLE OF INVENTION: HUVCT36  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,974A  
; FILING DATE: October 3, 1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG50022  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5024  
; TELEFAX: 610 270 5090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1597  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: No  
US-08-724-974A-1

Query Match 11.8%; Score 110; DB 2; Length 1597;  
Best Local Similarity 50.2%; Pred. No. 2e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
QY 87 CCTGCTGTGTAGGCTGCTCTCAACAGCTGCGGCTCTGGGTGTTCTGCTGCGCAT 146  
DB 431 CGTGTGTGTGGGCTTCCCGGCAACTGCTGCTGCTCTACTTCCGCTACTCGGCTAC 490  
QY 147 GCAGCAGTGGACGAGACCCGCTATCTACATGACCAACTGGCGGTGGCGGACCTCTG 206  
DB 491 CAGGCCCGGACAGCTGGGCGGTACTGTGCAACTGACGGTGGCGGACCTCTTCTA 550  
QY 207 GCTGTGACCTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266  
DB 551 CATCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610  
QY 267 CCAGCTTCCAGGGCATCTACCTGACC-----AACAGGTACATGAGCATCAG 314

Db 611 CGACCTGCTCCGCGAGTGTGGGCATCCTCTGTACGAGAACATCTACATCAGCGTGG 670  
Qy 315 CTTGCTCAGCGCATCGCGTGGACCGCTATGTGCGCGTGGCGACCGCTGCGTGGCGCG 374  
Db 671 CTTCTCTGTGCTCATCTCCGTGGACCGCTACTGTGCTGTGGCCCATCCCTCCGTTCCA 730  
Qy 375 CGGCGTGGCGTCCCCAGCAGCTGCGGCGGTGTGCGCGTCTCTGGG-----T 425  
Db 731 CCAGTTCCGACCCCTGAAGCGCGCTGCGCGTCAAGCTGTGTCATCTGGCCCAAGAGCT 790  
Qy 426 GCTGTCTATCGGCTCCCTGGTGGCTGCTGGGATTCAGAGGCGGCTTCTG 485  
Db 791 GCTGACCAAGCATCTCTCTGATGACAGAGAGGTCTATCGAGGACGAGAACAGACCG 850  
Qy 486 CTTTCAAGAGCACCGGCAAAATTCAACTCCATGCGGTTCCCGCTGCTGGGATTTACT 545  
Db 851 CGTGTCTTTGAGCACTACCCCATCCAGGCATGGCAGCGCGCATCAACTACTACCGCTT 910  
Qy 546 GCCCTTGGCGGTGGTCTTCTGTCTCCCTGAAGGTGGTGACTGCCCTGGCCCGAGAGCC 605  
Db 911 CTTGTTGGGCTTCTCTTCCCATCTGCTGTGCTGTGGGTCTTACCAGGCGATCCTGG 970  
Qy 606 ACC-----ACGAGTGGGCGAGCAGAGCGCACCCGCAAGGTAAACGATGTT 656  
Db 971 CGCGTGGCGCGAGCACCGCACCCAGAAAGCGCGCAAGGACCAAGATCCAGCGGTGT 1030  
Qy 657 CTGGGCAACTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 716  
Db 1031 GCTCAGCACCGTGGTCACTTCTGCGCTGCTTCTGCGCTTCTGCGCTTACCAGGT 1090  
Qy 717 GCGCTCTGCGAGTGGGCTGGAACGCTGTGCTCTCTGAGAGAGTCCGTCGCGCTGTA 776  
Db 1091 GCGCAGC---GTCTGGAGCGCAGCTGCGACTTCCCAAGGGGTTTCAACGCTACCA 1147  
Qy 777 CATAACCAAGCAAGCTCTCAGATGCCAACTGCTGCTGGACGCCATCTGCTACTACTAT 836  
Db 1148 CTTCTCCCTCTCTCACCAGCTTCAACTGCGTGGCGGACCGCTGCTACTGCTTCT 1207  
Qy 837 GCGCAAGGATTCAGGAGG 856  
Db 1208 CAGCGAGACCCACCCCGG 1227

## RESULT 9

US-09-364-425B-26  
; Sequence 26, Application US/09364425B  
; Patent No. 6653086  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Chen, Ruoping  
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor  
; FILE REFERENCE: Aren0047  
; CURRENT APPLICATION NUMBER: US/09/364,425B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/094,879  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/106,300  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 60/110,906  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 1697  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-364-425B-26

Query Match 11.8%; Score 110; DB 4; Length 1697;  
Best Local Similarity 50.2%; Pred. No. 2,1e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
Qy 87 CTTGCTGTGTGAGCCTGTCTCAACAGAGCTGCGGTCTGTGGGTGTCTGTGTCGCGAT 146  
Db 413 CTTGCTGTGTGAGCCTGTCTCAACAGAGCTGCGGTCTGTGGGTGTCTGTGTCGCGAT 472  
Qy 147 GCAGCAGTGGAGGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGGCTCTGCT 206  
Db 473 CAAGCCCGGAACAGAGCTGGGCGGTACTGTGTCAACCTGACGGTGGCGGACCTCTCT 532  
Qy 207 GCTGTGACCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266  
Db 533 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592  
Qy 267 CAGCTCTCCAGGCGCATCTACTGACC-----AACAGGTATAGAGATCAG 314  
Db 593 CGACCTGCTCTGCGAGGTGTGCGCATCTCTCTGTACGAGAACATCTATCAGCGTGG 652  
Qy 315 CTTGCTCAGGCGCATCGCGGTGGACCGCTATGTGCGCGTGGCGACCGCTGCTGCGCG 374  
Db 653 CTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712  
Qy 375 CGGCTGCGGTCTCCCGAGGCGTGGCGGTGTGCGCGTCTCTTGGG-----T 425  
Db 713 CAGTTCCGACCCCTGAAGCGCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772  
Qy 426 GCTGTCTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485  
Db 773 GCTGACCAAGCATCTACTTCTGATGACAGAGGTCTATCGAGGACGAGAACAGCACCG 832  
Qy 486 CTTCAGGAGCACCGCGCAATTTCAACTCCATCGGTTTCCCGTCTGGGATTTCTACT 545  
Db 833 CTTGCTGCTTTGAGCACTACCCCATCCAGGCGATGGCAGCGCGCATCAACTACTAC 892  
Qy 546 GCGCTGCGGTGCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605  
Db 893 CTTGCTGCTTCT 952  
Qy 606 ACC-----ACCGAGCTGGGCGAGGCGCAGAGGCGCACCCCAAGGTAAACGATGTT 656  
Db 953 CGCGTGGCGGAGCGCACCGCACCAAGAGCGCGCAAGGACAGATCCAGCGGTGTT 1012  
Qy 657 CTGGGCGCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716  
Db 1013 GCTCAGCACCGTGGTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072  
Qy 717 GCGCTCTGCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776  
Db 1073 GCGCAGC---GTCTGGAGGCGAGTGGAGTTCGCAAGGGGTTTCAACGCGCTACCA 1129  
Qy 777 CATAACCAAGCAGCTCTCAGATGCCAACTGCTGCTGGACGCCATCTGCTACTACTAT 836  
Db 1130 CTTCTCCCTCTCTCTCACCAGCTTCAACTGCGTGGCGGACCGCGTCTCTACTGCT 1189  
Qy 837 GCGCAAGGATTCAGGAGG 856  
Db 1190 CAGCGAGACCCACCCCGG 1209

## RESULT 10

US-09-170-496D-165  
; Sequence 165, Application US/09170496D  
; Patent No. 655339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein Receptor  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040

```

; CURRENT APPLICATION NUMBER: US/09/170,496D
;
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-165

```

Query Match 11.8%; Score 109.6; DB 4; Length 1089;  
Best Local Similarity 52.5%; Pred. No. 2.3e-15;  
Matches 272; Conservative 0; Mismatches 234; Indels 12; Gaps 1;

98	QY	TAGSCTGTGCTCAACAGCCTGGCGCTCTGGGTGTTCTGTGCGCGCATGACAGCAGTGA	157
89	Db	TGGGGCTGCCACCAATGCTGCTGGCTCTGTGGCGGCGCTACCGCCAGGTGCAACAGCGCA	148
158	QY	CGGAGACCCGCATCTACATGACCAACTGGCGGTGGCGGACCTCTGCCCTGTGTGTGCACCT	217
149	Db	ACGAGCTGGGCGCTCTACTGATGAACCTCAGCATGCGCGACCTGTGTACATCTGCACGC	208
218	QY	TGCCCTTGTGTCTCACTCCCTCGGAGAC-----ACCTCAGACACGCGCGTGT	265
209	Db	TGCCGTGTGGTGGACTACTTCTGCACCAAGCAACTGATCCACGGCCCGGGTCTCT	268
266	QY	GCCAGCTCTCCACGGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTCACGG	325
269	Db	GCAAGCTCTTTGGGTTCATCTTCTACACCAATATCTACATCAGCATCGCCTTCTCTGTCT	328
326	QY	CCATTCGCGGTGACCGGTATATGTGGCGGCGGACCCCGCTGGTGCCCGCGGCTGCGGT	385
329	Db	GCATCTCGGTGGACCGGTACCTGGCTGTGGCGCCACCCCACTCGCTTCGCGCGCTGCGCC	388
386	QY	CCCCACGACGGCTCGCGCGGTGTGGCGGTCTCTGGGTGCTGTGTATCGGCTCCCTGG	445
389	Db	CGGTCAAGACCGCCGTGGCGGTGAGTCCGTGGTCTGGGCGCACGGAGCTGGGCGCGCACT	448
446	QY	TGGTCTGCTGCTCTCTGGGATTCAGGAGGCGGCTTCTGTTCAGGAGCACCCGGCACA	505
449	Db	CGGCGGCCCTGTTCATGACGAGCTCTTCGAGACCGCTACAAACACACTTCTGCTTTG	508
506	QY	ATTTCAACTCCATCGGTTCCCGCTGTGGGATTCATCTGCCCTCGGCGGTGTGTGCT	565
509	Db	AGAAGTCCCAATGGAAGGCTGGGTGGCTGGATGAACCTCTATCGGGGTGTCTGTGGCT	568
566	QY	TCTGCTCCCTGAAGGTGTGACTGCCCTGGCCCCAGG	603
569	Db	TCCTCTTTCCGTGGCGGCTCATGTGCTGTGTGTGTACCGG	606

## RESULT 11

```

RESOLUTION 11
; US-09-170-496D-193
; Sequence 193, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endog
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-193

```

Query Match 10.0%; Score 92.6; DB 4; Length 1128;

	Best Local Similarity	47.9%;	Pred. No. 1.5e-11;	
	Matches	371;	Conservative	0; Mismatches 389; Indels 15; Gaps 3;
Qy	66	CTTCTACGGCTACTTGGGGGTCTCTGTGTGGTCTAGGCCTCTGCTCAACAGCCTGGCGCT	125	
Db	183	CTCGTGCCCTACACCATCTTCTCTTCCCATCGGCTTGTGGCAACATCCTGATCCT	242	
Qy	126	CTGGGTGTTTGTCTGGCGCATGACAGATGGAGCGGAGACCCGGATCTACATGACCAACCT	185	
Db	243	GGTGTGGAACATCAGCTTCCGCAGAAGATGACCATCCCGACCTGTACTTTCATCAACCT	302	
Qy	186	GGCGGTGGCGACCTCTGCTGCTGTGCACTTGGCCCTGCTGCTGTCACCTCCCT	239	
Db	303	GGCGGTGGCGACCTCATCTCTGTGGCGGACTCCCTCATTTAGGTGTTCAACCTGCAACGA	362	
Qy	240	GGGAGACACTCTAGACACCGCGCTGTGCCAGCTCTCCCAAGGGATCTTACCTGACCAACAG	299	
Db	363	GGGTACTAGACATCGCGCTCTGTGCACCTTCATGTGCTCTTCTCGAGGTCAACAT	422	
Qy	300	GTCATGAGCATCAGCCTGGTTCACGGCCATCGCCGTGGACCGCTATGTGGCCCTGGGCA	359	
Db	423	GTACAGCAGCGTCTTCTTCTCACCCTGGATGAGCTTCGACCGCTACATCGCCCTGGCCAG	482	
Qy	360	CCGCTGTGGTGGCCGGGGTGGGTTCCCGCAGGAGGCTCGCGCGTGTGGCGGTCCT	419	
Db	483	GGCCATCGCTGCAGCCTGTTCGCGCACCAAGCACCGCCGGCTGAGCTGTGGCCTCAT	542	
Qy	420	CTGGGTGCTGGTCATCGGCTCCCTGTGTGGCTCGCTGGCTCTCGGGATTCAGAGAGGCGG	479	
Db	543	CTGGATGGCATCCGTGTACGCCACGCTGTGTGCCCTTTCACCGCCGTGCACCTGCAGACAC	602	
Qy	480	CTTCTGCTTCAGAGACACCGGCACAAATTTCAAATCCATGCGGTTCGCCG	533	
Db	603	CGACGAGGCTGCTTCTGTTCGCGGATGTCCGGGAGGTGCATGGCTCGAGGTCAAGCT	662	
Qy	534	GGAAATCTACTGCCCTCGCCGTGTGTGTCTTCTGTCTCCCTGAAAGGTGTGATCTGCCCT	593	
Db	663	GGGCTTCATCTGTGCCCTTGCCCATCATCGCCCTGTGTCTACTCCCTCATTTCTCGGGTGT	722	
Qy	594	GGCCACAGAGCCACCCACGACGTGGGGCAGGACAGGGCCACCCGGCAGAGCTAAACGCAT	653	
Db	723	GGTCT--AGGGCGCACCGGACCGTGGGCTGGCGGCCCGCGGACAGAGCGAAACGCAT	779	
Qy	654	GGTCTGGGCAACCTCTCTGTGTGTCTGTGTGTCTTCTTCTGCCCTTGACAGCTGGGCTGAC	713	
Db	780	GATCTCTGGGTGGTGTGTCTTCTTCTGTCTGTGTCTGTGTCTGTGTGTGTGTGTGTGTGT	839	
Qy	714	AGTGGCCCTCGCAGTGGGCTGGAAACCGCTGTGCCCTCTCTGGAGACGATCCGTGCGGCCCT	773	
Db	840	CGTGGACCTCTGCAGGGACCGACGCTGGGGCGGCTCCCTGCAAGCAGTCTTTTCGCCCA	899	
Qy	774	GTACATAACAGCAAGCTCTCAGATGCCAACTGCTGCTGGAGCCCATCTGTCTAC	828	
Db	900	TGCCCAACCCCTCAGCGGGCCACATTTGTTCAACCTTCGCGGCTTCTCCAAACAGCTGC	954	

## RESIT.T 12

```

RESOLUTION 12
US-09-170-496D-201
; Sequence 201, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 201
; LENGTH: 1128

```





Db 1241 GCCTCTGCTGGTTCATCAGCGTGTTCACCGCCGCGCATCAT-GTGTGCACTGTTCGCGCGCG 1299  
QY 585 GACTGCCCTGGCCAGAGCCACCCACGACGTGGGGCAGGAGGCCACCCGCAAGGC 644  
Db 1300 GTCTGCTCGCCAGGCTCGCCAGCGCGGTCGCGGCCCATGCACTCTCTGCTCACGGTGC 1359  
QY 645 TAAAC 649  
Db 1360 TCATC 1364

## RESULT 14

US-09-327-925-1

; Sequence 1, Application US/09327925A

; Patent No. 6096868

; GENERAL INFORMATION:

; APPLICANT: SATHE, GANESH M.

; APPLICANT: HALSEY, WENDY S.

; APPLICANT: MAO, JOYCE YUE

; TITLE OF INVENTION: ECR673: A 7 TRANSMEMBRANE G-PROTEIN

; FILE REFERENCE: GP-70414-1

; CURRENT APPLICATION NUMBER: US/09/327,925A

; EARLIER FILING DATE: 1999-06-08

; EARLIER APPLICATION NUMBER: 09/041,545

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 1815

; TYPE: DNA

; ORGANISM: HOMO SAPIENS

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (16)

US-09-327-925-1

## Query Match

Best Local Similarity 9.8%; Score 91; DB 3; Length 1815;

Matches 305; Conservative 50.4%; Pred. No. 3.8e-11;

Matches 305; Conservative 0; Mismatches 290; Indels 10; Gaps 3;

QY 48 CCCAGCATCAAGCTGGGCTTCTAGCCTACTTGGGGCTCTGCTGGTGTAGGCTGCT 107  
Db 767 CCCAGGCTGTGGCTGGCGCTGATGCGGCTGACGAGGCCAATCTCTGGCAGGGCTGT 826  
QY 108 GCTCAACAGCTGGCGCTCTGGGTGTCTGTGCGCATGACAGTGGACGAGACCG 167  
Db 827 GCTCAACGGCTGGCGCTGTAGCTCTTCTGTGCGCGACCCGGGCAAGACACCTCAGT 886  
QY 168 CATCTACATGACCAACCTGGCGGTGGCGACCTCTGCGCTGTGTGCACCTTGGCTTGGT 227  
Db 887 CATCTACACCATCAACCTGGTGTGACCGATCTACTGTGTAGGCTGTCCCTGCCACCGG 946  
QY 228 GCTGCACCTCCGCGAGACACCTCAGACACGCGCTGTGTGCCAGCTCTCCAGGGATC-- 285  
Db 947 CTTGCTGTGTACTACGGCGCCAGGGGCTGCTTGGCGCTGTGCTTCCCGCACGTCTCGG 1006  
QY 286 -TACCTGACCAACAGTACATGACATCAGCTGTGTCAAGGCTTCCGCGCATCGCGTGGACGCTA 344  
Db 1007 TTACTTCTCAACATGCACTGTCTCCTCTTCTCTCACTGCACTGTGGTGGACCGCTA 1066  
QY 345 TGTGCGCGTGGCGCACCCGCTGCTGCTGCCGCGGGTGGCGGTCCCGCAGGAGCTGCGGC 404  
Db 1067 CTTGGCCATCTGTGCGGCTTGAAGGCTCCGCGCTGCCCGCAGCTGCTGTGCCAGGC 1126  
QY 405 CGTGTGCGGCTCTCTGCGGTCTGGTTCATCGGCTCCCTGTGTGGTGTGCTCTCTGG 464  
Db 1127 CGTGTGCGCTTCTGCTGTGGCTGGCGCGGTGCC-----GTCAACCTGTCTGGTGTGG 1180  
QY 465 GATTTCAGGAGGGCGCTTCTGCTTTCAGGAGCACCCGCGACATTTCAACTCCATCGGTT 524  
Db 1181 CGTGACAGGACCGCGCTCTGCTGCGGTGTCTTTGCGGTGACTGTCTTCTGCT 1240

Search completed: May 23, 2005, 14:02:30

Job time : 209 secs

QY 525 CCCGCTGTGGATTTCTACCTGCCCTTGGCGTGTGTGCTTCTGCTCCCTCAAGGTGT 584  
Db 1241 GCCTCTGCTGGTTCATCAGCGTGTTCACCGCCGCGCATCAT-GTGTGCACTGTTCGCGCGCG 1299  
QY 585 GACTGCCCTGGCCAGAGCCACCCACGACGTGGGGCAGGAGGCCACCCGCAAGGC 644  
Db 1300 GTCTGCTCGCCAGGCTCGCCAGCGCGGTCGCGGCCCATGCACTCTCTGCTCACGGTGC 1359  
QY 645 TAAAC 649  
Db 1360 TCATC 1364

## RESULT 15

US-09-826-509-574

; Sequence 574, Application US/09826509

; Patent No. 6806054

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: Patentin Version 2.1

; SEQ ID NO 574

; LENGTH: 1167

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-574

## Query Match

Best Local Similarity 9.6%; Score 89; DB 4; Length 1167;

Matches 217; Conservative 55.5%; Pred. No. 9.6e-11;

QY 45 GCCCCAGCGATCAAGCTGGGCTTCTACGCTTACTTGGGCGTCTGCTGTAGGCTT 104  
Db 126 GCGGCGCGCGCGCATGTGCTATCCAGTGCACTTACGCGTGTGTGCTTGGTGGGCT 185  
QY 105 GCTGCTCAACAGCTGGCGCTTGGTGTCTGTGCGCATGACGAGTGGACGAGAC 164  
Db 186 GGTGGGCAACGCGCTGGTCACTTCTGATCTTTCGTACGCCAAGATGAAGACGGCTAC 245  
QY 165 CCGCATCTACATGACCAACCTGGCGGTGGCGGACCTCTGCGCTGTGTGCACCTTGGCTT 224  
Db 246 CAACATCTACTGCTCAACCTGGCGGTAGCGAGAGCTTCTTCACTGCTGAGGTGCTT 305  
QY 225 CGT-----GTGCACTCCCTGCGAGAC---ACCTCAGACACGCGCTGTGTGCACTCTC 275  
Db 306 GGTGCGCTCGTGGCGCGCCCTCGGCCACTGGGCCCTTTCGGCTCGCTGTGTGCGCGCT 365  
QY 276 CCAGGGCATCTTACCTGACCAACAGGTATGAGCATCAGCTGGTGTGCGGCTATCGGCT 335  
Db 366 GCTCAGCGTCAACGCGCTCAACATGTTTCAACGCGTCTTCTGCTCAGCGTCTCAGCT 425  
QY 336 GGACCGTATGTGGCGGTGGCGCACCCGCTGTGTCGCCGCGGCTGCGTCCCGCAGGCA 395  
Db 426 GGACCGCTTACGTGGCGGTGGTGCACCTCTTGGCGCGGGGACCTACCGGCGGCCAGCT 485  
QY 396 GGTGCGCGCGGTGTGCGGCTTCTCTGGGTG 426  
Db 486 GGCCAAAGCTCATCAACCTGGGCGTGTGCTG 516



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.  
OM protein - protein search, using sw model  
Run on: May 23, 2005, 11:09:25 ; Search time 58.5 Seconds  
(without alignments)  
2704.829 Million cell updates/sec  
Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKAHKSQSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1608	99.6	309	1 GP35_HUMAN	Q9hc97 homo sapien
2	1602	99.3	394	2 Q6ZMP9	Q6zmp9 homo sapien
3	1124	69.6	307	1 GP35_MOUSE	Q9es90 mus musculus
4	1123	69.6	307	2 Q8CB97	Q8cb97 mus musculus
5	1109	68.7	307	2 Q8BS98	Q8bs98 mus musculus
6	402	24.9	370	1 P2Y9_HUMAN	Q99677 homo sapien
7	400	24.8	370	2 Q6NSP5	Q6nsp5 homo sapien
8	400	24.8	370	2 Q8BKK1	Q8bkk1 mus musculus
9	392	24.3	370	2 Q8BLG2	Q8blg2 mus musculus
10	376	23.3	319	2 Q8N580	Q8n580 homo sapien
11	375.5	23.3	363	2 Q8TDS4	Q8tds4 homo sapien
12	368.5	22.8	308	1 P2Y5_CHICK	P32250 gallus gall
13	368.5	22.8	387	1 Q9B9_HUMAN	P49019 homo sapien
14	368.5	22.8	387	2 Q8NGE4	Q8nge4 homo sapien
15	368	22.8	347	2 Q7ZA4	Q7zza4 brachydanio
16	365.5	22.6	296	2 Q9WU09	Q9wu09 rattus norv
17	362	22.4	372	1 GP92_HUMAN	Q9nlc0 homo sapien
18	361.5	22.4	344	1 P2Y5_HUMAN	P43657 homo sapien
19	361.5	22.4	344	2 Q7Z3S0	Q7z3s0 homo sapien
20	361.5	22.4	344	1 P2Y3S6	Q7z3s6 mus musculus
21	357.5	22.1	344	1 P2Y5_MOUSE	Q8bmc0 mus musculus
22	348.5	21.6	360	2 Q9EP66	Q9ep66 mus musculus
23	340	21.1	319	2 Q9Y2T6	Q9y2t6 homo sapien
24	338.5	21.0	360	2 Q80Z39	Q80z39 rattus norv
25	331.5	20.5	374	1 P2Y2_RAT	P41232 rattus norv
26	331	20.5	298	2 Q8VE54	Q8ve54 mus musculus
27	330.5	20.5	377	1 P2Y2_HUMAN	P41231 homo sapien
28	327	20.3	346	1 GP81_HUMAN	Q9bxc0 homo sapien
29	324	20.1	346	2 Q6NXU5	Q6nux5 homo sapien
30	322.5	20.0	345	1 CLT2_PIG	Q95n03 sus scrofa
31	321	19.9	349	2 Q6P852	Q6p852 xenopus tro

RESULT 1									
ID	GP35_HUMAN	STANDARD;	PRT;	309	AA.				
AC	Q9HC97; O43495; Q86UH4;								Q8cl31 mus musculus
DT	16-OCT-2001 (Rel. 40, Created)								O35811 rattus norv
DT	29-MAR-2004 (Rel. 43, Last sequence update)								Q63371 rattus norv
DT	25-OCT-2004 (Rel. 45, Last annotation update)								P35383 mus musculus
DE	Probable G protein-coupled receptor GPR35.								P34996 gallus gall
GN	Name=GPR35;								P49652 meleagris g
OS	Homo sapiens (Human).								O57466 meleagris g
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								Q9ns75 homo sapien
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								Q924t9 rattus norv
OX	NCBI_TaxID=9606;								Q9jjs7 mus musculus
RN	[1]								P51582 homo sapien
RP	SEQUENCE FROM N.A.								P25023 rattus norv
RX	MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;								Q684m8 homo sapien
RA	O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,								P30411 homo sapien
RA	Heng H.W.Q., Kolakowski L.F. Jr., George S.R.;								
RT	"Discovery of three novel G-protein-coupled receptor genes.";								
RL	Genomics 47:310-313(1998).								
RN	[2]								
RP	SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;								
RP	MET-253 AND SER-294.								
RX	MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;								
RA	Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,								
RA	Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,								
RA	del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,								
RA	Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,								
RA	Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,								
RA	Bell G.I.;								
RT	"Genetic variation in the gene encoding calpain-10 is associated with								
RT	type 2 diabetes mellitus.";								
RL	Nat. Genet. 26:163-175(2000).								
RN	[3]								
RP	SEQUENCE FROM N.A., AND VARIANT SER-294.								
RA	Warren C.N., Aronstam R.S., Sharma S.V.;								
RT	"cDNA clones of human proteins involved in signal transduction								
RT	sequenced by the Guthrie cDNA resource center (www.cdna.org).";								
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.								
CC	!- FUNCTION: Orphan receptor.								
CC	!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).								
CC	!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues								
CC	examined, including pancreatic islets and skeletal muscle, with								
CC	relatively higher levels in adult lung, small intestine, colon and								
CC	stomach.								
CC	!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.								
CC	-----								
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation								
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CC	modified and this statement is not removed. Usage by and for commercial								
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								

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CC EMBL; AF027957; AAC52028.1; --
DR EMBL; AF089087; AAG17965.1; --
DR EMBL; AF275467; AAP32299.1; --
DR Genew; HGNC:4492; GPR35.
DR MIM; 602646; --
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT DOMAIN 1 24 Extracellular (Potential).
FT TRANSMEM 25 45 1 (Potential).
FT DOMAIN 46 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 90 Extracellular (Potential).
FT TRANSMEM 91 112 3 (Potential).
FT DOMAIN 113 135 Cytoplasmic (Potential).
FT TRANSMEM 136 156 4 (Potential).
FT DOMAIN 157 174 Extracellular (Potential).
FT TRANSMEM 175 195 5 (Potential).
FT DOMAIN 196 218 Cytoplasmic (Potential).
FT TRANSMEM 219 239 6 (Potential).
FT DOMAIN 240 258 Extracellular (Potential).
FT TRANSMEM 259 279 7 (Potential).
FT DOMAIN 280 309 Cytoplasmic (Potential).
FT DISULFID 89 162 By similarity.
FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
FT VARIANT 25 25 A -> T.
FT VARIANT 29 29 /FTID=VAR_013601.
FT VARIANT 29 29 V -> I.
FT VARIANT 108 108 /FTID=VAR_013602.
FT VARIANT 108 108 T -> M.
FT VARIANT 125 125 /FTID=VAR_013603.
FT VARIANT 125 125 R -> S.
FT VARIANT 253 253 /FTID=VAR_013604.
FT VARIANT 253 253 T -> M.
FT VARIANT 294 294 /FTID=VAR_013605.
FT VARIANT 294 294 R -> S.
FT CONFLICT 174 174 A -> R (in Ref. 1).
FT SEQUENCE 309 AA; 34141 MW; FC034PB7231B26F1 CRC64;

Query Match 99.6%; Score 1608; DB 1; Length 309;
Best Local Similarity 99.7%; Pred. No. 7.5e-114;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQWTETRIYMT 60
DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQWTETRIYMT 60
QY 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDYVAVRH 120
DB 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDYVAVRH 120
QY 121 PLRARGLRSPROAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLLG 180
DB 121 PLRARGLRSPROAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLLG 180
QY 181 YLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVWVWVNVVVCFLPLHGLTVR 240
DB 181 YLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVWVWVNVVVCFLPLHGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYNMAKEFOEASALAVAPRAKAHKS 300
DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYNMAKEFOEASALAVAPRAKAHKS 300
QY 301 QDSLVCVTLA 309
DB 301 QDSLVCVTLA 309
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RESULT 2
Q6ZMP9
ID Q6ZMP9 PRELIMINARY; PRT; 394 AA.
AC Q6ZMP9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16773.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDSB databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK131540; BAD18676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 394 AA; 43308 MW; 1598FD44BAE4233C CRC64;

Query Match 99.3%; Score 1602; DB 2; Length 394;
Best Local Similarity 99.4%; Pred. No. 2.6e-113;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQWTETRIYMT 60
DB 86 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQWTETRIYMT 145
QY 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDYVAVRH 120
DB 146 NLAVADLCCLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYMSISLVTAIAVDYVAVRH 205
QY 121 PLRARGLRSPROAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLLG 180
DB 206 PLRARGLRSPROAAACAVLVWLVGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLLG 265
QY 181 YLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVWVWVNVVVCFLPLHGLTVR 240
DB 266 YLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVWVWVNVVVCFLPLHGLTVR 325
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYNMAKEFOEASALAVAPRAKAHKS 300
DB 326 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYNMAKEFOEASALAVAPRAKAHKS 385
QY 301 QDSLVCVTLA 309
DB 386 QDSLVCVTLA 394

RESULT 3
GP35_MOUSE
ID GP35_MOUSE STANDARD; PRT; 307 AA.
AC Q9ES90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RL sequencing pipeline with 384 multicapillary sequencer.";   
RN Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RC TISSUE=Embryonic body between diaphragm region and neck;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanaagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AK034870; BAC28861.1; -;  
DR MGD; MGI:1929509; Gpr35.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR002286; P2\_purinocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR01157; P2PURNOCPTR.  
DR PRINTS; PR00237; GPCRHOODPSN.  
DR PROSITE; PS00237; G-PROTEIN RECEPT\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPT\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;  
  
Query Match 68.7%; Score 1109; DB 2; Length 307;  
Best Local Similarity 71.3%; Pred. No. 4.2e-76;  
Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;  
  
Qy 1 MNGVTNCGSDLTWPPAIKLGFAVLGVLLGLLNSLAWFCRCMQQWTEIRIYMT 60  
Db 1 MNST--TCNST-LTPASVNNFFIYSALLVIGLLNSVALWVFCYRHHQWTEIRIYMT 57  
  
Qy 61 NLAVADLCCLCTLPVLSLRL-DTSDDTLCQLSQGIYLTNRYSISLVTALVDRIYAVR 119  
Db 58 NLAVADLCCLCSLPVLSLKYSSSDTPVCQLSQGIYLTNRYSISLVTALVDRIYAVR 117  
  
Qy 120 HPLRARGLRSPQAAACAVLWLVIGSLVARWLLGIQEGGFCFRS-TRHNFNSMRPFL 178  
Db 118 HPLRARELRSPQAAACVAVLWVIVTSLVVRWRLGMQEGGFCFSSTRRNPFSTAFSLL 177  
  
Qy 179 GFYPLAVVFCSLKVTALAQRPPTVQQAETFKAAWYWANLLVFVFCFLPHVGLT 238  
Db 178 GFYPLAVVFCSLQVTVLRRPADVQGAETQKATHWVANLAVFVICFLPHVGLT 237  
  
Qy 239 VRLVAGWNCALLETIRRALYITTSKLSANCCCLDAICYYVMAKEFQEAASALAVAPRAKH 298  
Db 238 VOVSNLNLTCAARDTFSRALSITGKLSNTNCLDAICYYVMAKEFQEAATSSNT-PH 296  
  
Qy 299 KQPSLQCVLT 308  
Db 297 KQVQSILSL 306  
  
RESULT 6  
ID P2Y9 HUMAN STANDARD; PRT; 370 AA.  
AC Q99677; O15132;  
DT 01-NOV-1997 (Rel. 35; Created)  
DT 01-NOV-1997 (Rel. 35; Last sequence update)  
DT 25-OCT-2004 (Rel. 45; Last annotation update)  
DE P2Y purinoceptor 9 (P2Y9) (Purinerigic receptor 9) (G protein-coupled

DE receptor GPR23) (P2Y5-like receptor).  
GN Name=GPR23; Synonyms=P2RY9;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97225799; PubMed=9073069; DOI=10.1016/S0378-1119(96)00722-6;  
RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,  
RA Kolakowski L.F. Jr., Lynch K.R., George S.R.;  
RT "Cloning and chromosomal mapping of four putative novel human G-  
RT protein-coupled receptor genes.";   
RL Gene 187:75-81(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bohm S.K., Kilitin L.M., Payan D.P., Bunnett N.W.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97366605; PubMed=9223435; DOI=10.1006/bbrc.1997.6895;  
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;  
RT "Cloning of a human heptahelical receptor closely related to the P2Y5  
RT receptor";   
RL Biochem. Biophys. Res. Commun. 236:106-112(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";   
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Bird C.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,  
CC putamen, caudate, frontal cortex, pons, hypothalamus and  
CC hippocampus.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; U66578; AAC51301.1; -;  
DR EMBL; U90323; AAB62087.1; -;  
DR EMBL; U90322; AAB62088.1; -;  
DR EMBL; AF005419; AAB66322.1; -;  
DR EMBL; AY301274; AAP58404.1; -;  
DR EMBL; AL590083; CAD18851.1; -;  
DR FIR; JC5549; JC5549.  
DR HSSP; P34996; 1DDD.  
DR Genes; HGNC:4478; GPR23.  
DR MIM; 300086; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR InterPro; IPR002188; P2Y5\_purinocptor.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOODPSN.  
DR PROSITE; PS00237; G-PROTEIN RECEPT\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPT\_F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
FT DOMAIN 1 43 Extracellular (Potential).  
FT TRANSMEM 44 64 1 (Potential).  
FT DOMAIN 65 73 Cytoplasmic (Potential).  
FT TRANSMEM 74 94 2 (Potential).

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FT DOMAIN          95 112 Extracellular (Potential).
FT TRANSMEM       113 133 3 (Potential).
FT DOMAIN         134 155 Cytoplasmic (Potential).
FT TRANSMEM       156 176 4 (Potential).
FT DOMAIN         177 203 Extracellular (Potential).
FT TRANSMEM       204 224 5 (Potential).
FT DOMAIN         225 254 Cytoplasmic (Potential).
FT TRANSMEM       255 275 6 (Potential).
FT DOMAIN         276 294 Extracellular (Potential).
FT TRANSMEM       295 315 7 (Potential).
FT DOMAIN         316 370 Cytoplasmic (Potential).
FT DISULFID       111 188 By similarity.
FT CARBOHYD       15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       183 183 N-linked (GlcNAc...) (Potential).
FT CONFLICT       192 192 F -> L (in Ref. 3).
SQ SEQUENCE       370 AA; 41895 MW; 20857F52A3929E48 CRC64;

Query Match          24.9%; Score 402; DB 1; Length 370;
Best Local Similarity 34.1%; Pred. No. 1.5e-22;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLNSLALWVFCRCMQQWTTETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVSVVVFILGLITNSVLSVFCFRMKMRSETAIFTINLAVSDLLFVCTLPFKIFYNFNRH 103

QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFITNIYSGMLFLTCISVDRLAIVYFPRSTIRTRNSAIVCAGV 162

QY 141 WVLVTGSLVARMLGIQE-----GGFCFRSTRHNFSMR--FPLLGFLPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKTKYLSKITIFIEVVGFIIPLINVS 222

QY 190 CSLKVVVTAALQRPPTDVGQAEAT-RKAARMVWVANLLVFVVCFLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVLMITHMAVVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCLDAICYYYMAKEQFASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCATLNCPCDFPIIYFTLESFQKSFVI-----NAHRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 7
Q6NSP5
ID Q6NSP5 PRELIMINARY; PRT; 370 AA.
AC Q6NSP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE G protein-coupled receptor 23.
GN Name=GPR23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN TISSUE=PCR rescued clones;
RC Strausberg R.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
RL EMBL; BC069996; AAH69996.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:intrigueric nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002188; P2Y5_purinocptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PRINTS; PR01067; P2Y5ORPHANR.
DR PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; UNKNOWN 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW Receptor.
SQ SEQUENCE 370 AA; 41867 MW; 2AB4B3F5F43FFF83 CRC64;

Query Match          24.8%; Score 400; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 2.2e-22;
Matches 103; Conservative 59; Mismatches 112; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLNSLALWVFCRCMQQWTTETRIYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVSVVVFILGLITNSVLSVFCFRMKMRSETAIFTINLAVSDLLFVCTLPFKIFYNFNRH 103

QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFITNIYSGMLFLTCISVDRLAIVYFPRSTIRTRNSAIVCAGV 162

QY 141 WVLVTGSLVARMLGIQE-----GGFCFRSTRHNFSMR--FPLLGFLPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKTKYLSKITIFIEVVGFIIPLINVS 222

QY 190 CSLKVVVTAALQRPPTDVGQAEAT-RKAARMVWVANLLVFVVCFLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVLMITHMAVVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCLDAICYYYMAKEQFASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCATLNCPCDFPIIYFTLESFQKSFVI-----NAHRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 8
Q6BKK1
ID Q6BKK1 PRELIMINARY; PRT; 370 AA.
AC Q6BKK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE enriched library, clone: D130067B12 product: P2Y PURINOCCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;

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OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK051709; BAC34729.1;  
 DR MGD; MGI:1925384; Gpr23.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G...; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR InterPro; IPR002188; P2Y5\_purinocptor.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHOOPS.N.  
 DR PRINTS; PR01067; P2Y5ORPHAN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPT\_F1.1; UNKNOWN\_1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPT\_F1.2; 1.  
 SQ SEQUENCE 370 AA; 41956 MW; ABI26B4234343A5E1 CRC64;  
 Query Match 24.8%; Score 400; DB 2; Length 370;  
 Best Local Similarity 34.3%; Pred.No. 2.2e-22;  
 Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;  
 QY 4 TYNTCGSDLTWPPAIKLGfy-AYLGVLVLLGLLNSLWVFCRCMQQWTTETRIYWNIL 62  
 DB 27 TNNTCIVDD-----SFKNLNGAVSVVFFLGLIINSASLFFVCFRMRSETAIFITNL 81  
 QY 63 AVADLCCLCTLPFF-VLHSLR---DTSDDLPCOLSGIYLTNRYMSISLTAIAVDYVAV 118  
 DB 82 ALSDLLFVCTLPFKIFYNFRHWPFGDT-LCKISGTAFLTNYGSMFLTCTISVDRLAI 140  
 QY 119 RHPLRARGLRSPQAAAVCNVLWLVIGSLVARWLLGQe-----GGFCFRSTRHN 169  
 DB 141 VYPPRSRTIRTRNSAIVCAGVWILVINGGISASLFTTNVNNATTTCEGFSKRVKTY 200  
 QY 170 FNSMR--FPLQGYLPLAVVFCSLKVVTAQAQRPPTDVGOAET-RKAARVWVANLLVF 226  
 DB 201 LSKITIFIEVVGFIPLILNWCSSVVLRTL--RKPATLSQIGTNKKVLMITVMAVF 258  
 QY 227 VVCFPLHVLTVRLAVGNAC--ALLETRDALY-ITSKLSDANCCCLDAICYYNMAKPF 283  
 DB 259 VVCFVYNSVFLYALVRSQAITNCLERFAKIMYPITLCLATLNCPCFPFIYFTLESF 318  
 QY 284 QEA 286  
 DB 319 QKS 321  
 RESULT 9  
 Q8BLG2 PRELIMINARY; PRT; 370 AA.  
 AC Q8BLG2;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130055L15 product:P2Y PURINOCEPTOR 9, full insert sequence.  
 GN Name=Gpr23;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]

RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [16]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saichoh K., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AK045289; BAC32299.1; -  
DR MGD; MGI:1925384; Gpr23.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. .; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR00276; GPCR Rhodopsin.  
DR InterPro; IPR002188; P215\_puroceptor.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; P2Y5ORPHAN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1\_1; UNKNOWN\_1.  
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1\_2; 1.  
SQ SEQUENCE 370 AA; 41872 MW; 0E4C79FEDFD32050 CRC64;  
Query Match 24.3%; Score 392; DB 2; Length 370;  
Best Local Similarity 34.5%; Pred. No. 8.8e-22;  
Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;  
QY 25 AVLGVLVLGLLNSLALVWFCRCMQWETRIYMTNLAVALDCLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGTLSSASLFVFCRCMKRSEITAFITNLALSLLFVCTLPFKIFYNFRH 103  
QY 82 -DTSDFPLCQLSQGIYLTNRYSISLVTAIVDVRVAVRHPLRARGLSRPROAAVCAVL 140  
DB 104 WFGDPT-LCKISGTAFGLTNIYGSMLFVLCISVDRLAIVYPRSRITRFRNSAIVCAGV 162  
QY 141 VWLVIGSLVARWMLLGIQE-----GGFCFRSTRHFNMSR--FPPLGLFVLPVAVVVF 189  
DB 163 WILVLSGGISASLSFTTNVNNATTTCEGFSKRVKMTYLSKITIFTEVVGVFIPLNLNS 222  
QY 190 CSLKVVVTAQAQRPPTDVGQAEAT-RKAARMVWNLVVFVCFPLHVLGTVRLAVGNAC 248  
DB 223 CSSWLVRLT--RKPATLSQIGTNKKKLVKMTIVHMAVVFVCFYFNYSVLFLVALVRSQAI 280  
QY 249 --ALLETIRRALY-ITSKLSANDCCLDAICYYNMAKEFQEA 286

DB 281 TNCLLERPAKIMYPITLCATLNCFCDFPIYFYFTLESFQKS 321  
RESULT 10  
Q8N580 PRELIMINARY; PRT; 319 AA.  
AC Q8N580;  
DT 01-OCT-2002 (TRENBLrel. 22, Created)  
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)  
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)  
DE G protein-coupled receptor 55 (GPR55 protein) (Fragment).  
GN Name=GPR55;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Gritwood J., Schmitt J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallic D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Halleck A., Ebert L., Mkomandya M., Schick M., Eisenstein S.,  
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., Labaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; BC032694; AAH32694.1; -  
DR EMBL; CF541776; CAG46575.1; -  
DR Genew; HGNC:4511; GPR55.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR00276; GPCR\_Rhodopsin.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1\_1; 1.  
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 319 AA; 36637 MW; D6B5C6CA8426E7D5 CRC64;  
Query Match 23.3%; Score 376; DB 2; Length 319;  
Best Local Similarity 36.9%; Pred. No. 1.3e-20;  
Matches 100; Conservative 44; Mismatches 103; Indels 24; Gaps 9;

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QY 32 VLGLLNSLALWVFC-----RMOQWETRIYMTNLAVADLCCLCTLPFVLHSLRDTSDTP 87
Db 32 VLGLLNLALHATGFTFLKRWDPEDVAATSIYINLAVFDLLVLPLPFWLWSQVSPFP 91
QY 88 -LCQLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVLVIV-I 145
Db 92 SLCTLVECLYFVSMYGSVFTICFISMDRELAIYPLVSHLSRPKIFGICCTIIVLWVT 151
QY 146 GSLVARWLLGIOGQCFRSTRHNFN-----SMRFPPL--LGFIYPLAVVFCSLKVTA 197
Db 152 GSIIPTYSFHGKVEKMYCF-----HNMSDDTWSAKVFPELVFGFLPLPMGIMGFCCSRSIHI 207
QY 198 LAQRPPTDVGQAEATFKAA-RMVWANLLVFFVCFPLHVLTVRLAVGWN-----ACALLET 253
Db 208 LLGR--RDHTQDWOOKACIYSIAASLAVFVVSFLPVLHGLGFLQLVLRNSFIVECRAKQS 265
QY 254 IRRALYITSKLSDANCCLDALCIYYWAKEFQ 284
Db 266 ISFFQLSCVFSNVNCLDVFYCYFVKEFR 296

RESULT 11
O8TDS4
ID Q8TDS4 PRELIMINARY; PRT; 363 AA.
AC Q8TDS4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE G protein-coupled receptor HM74a (Seven transmembrane helix receptor).
DE receptor.
DE Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takasue H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN 2;
RP SEQUENCE FROM N.A.
EX MEDLINE=2513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA Eilert M., Ignar D.M., Murdock P.R., Steplewski K., Green A.,
RA Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA Wilson S., Pike N.B.;
RT "Molecular identification of high and low affinity receptors for
RT nicotinic acid.";
RL J. Biol. Chem. 278:9869-9874 (2003).
RN 3;
RP SEQUENCE FROM N.A.
RA Elshourbagy N.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN 4;
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsuni S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB083632; BAB9345.1; -.
DR EMBL; AY148884; AAN71621.1; -.
DR EMBL; AB065876; BAC06094.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR002286; P2_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PRINTS; PR01157; P2YPURNOCPT.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41849 MW; C4B0EC9CCB81D56 CRC64;
Query Match 23.3%; Score 375.5; DB 2; Length 363;
Best Local Similarity 34.1%; Pred. No. 1.5e-20;
Matches 94; Conservative 48; Mismatches 107; Indels 27; Gaps 10;
QY 27 LGVLLVGLLLNSLALWVFCRMOQWETRIYMTNLAVADLCCLCTLPFVLHSL-----R 81
Db 34 LGLEFIFGLGLGLALWIFCFHLKSKSSRIFLNLAVADFLLIICLPFLMDNYVRRWDW 93
QY 82 DTSDFPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVLW 141
Db 94 KFGDTP-CRLMLFMLAMNRQSGIIFLTIVVADVRFVVRVPHHAKNISRTAAIISCLW 152
QY 142 VLIVGSLV--ARWLLGIOEGG--FCFR--STRHNF--NSMRFPPLGFIYPLAVVFCSLKV 194
Db 153 GITIGLTVHLLKKMPIONGGANLCSFSICHTFQWHEAMP-LLEFFFLPLGLIILFCSARI 211
QY 195 VTALAQRPTDVGQAEATFKAAARMVWANLLVFFVCFPLHVLTVRLAVGWN-----NA 247
Db 212 IWSLRQ---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQN 265
QY 248 CALLETIRRALYITSKLSDANCCLDALCIYYWAKEF 283
Db 266 CEVRSVDLAFITLFTSYMNSMLDPVVVYFSSPSF 301

RESULT 12
P2Y5_CHICK
ID P2Y5_CHICK STANDARD; PRT; 308 AA.
AC P32250;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
GN Name=P2Y5;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93329058; PubMed=8393036;
RA Kaplan M.H., Smith D.I., Sundick R.S.;
RT "Identification of a G protein coupled receptor induced in activated T
RT cells.";
RL J. Immunol. 151:628-636 (1993).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Induced in activated T-cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L06109; AAS06587.1; -.
DR FIR; I50241; I50241.
DR HSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR002188; P2Y5_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

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KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
KW Transmembrane.  
FT DOMAIN 1 16 Extracellular (Potential).  
FT TRANSMEM 17 43 1 (Potential).  
FT DOMAIN 44 52 Cytoplasmic (Potential).  
FT TRANSMEM 53 76 2 (Potential).  
FT DOMAIN 77 89 Extracellular (Potential).  
FT TRANSMEM 90 109 3 (Potential).  
FT DOMAIN 110 130 Cytoplasmic (Potential).  
FT TRANSMEM 131 151 4 (Potential).  
FT DOMAIN 152 178 Extracellular (Potential).  
FT TRANSMEM 179 206 5 (Potential).  
FT DOMAIN 207 224 Cytoplasmic (Potential).  
FT TRANSMEM 225 250 6 (Potential).  
FT DOMAIN 251 269 Extracellular (Potential).  
FT TRANSMEM 270 289 7 (Potential).  
FT DOMAIN 290 308 Cytoplasmic (Potential).  
FT CARBOHYD 5 5 N-linked (GlcNAc..). (Potential).  
FT LIPTD 281 281 S-palmitoyl cysteine (By similarity).  
FT DISULFID 86 165 Potential.  
SQ SEQUENCE 308 AA; 35597 MW; 4214E969633B6F7D CRC64;  
  
Query Match 22.8%; Score 368.5; DB 1; Length 308;  
Best Local Similarity 30.3%; Pred. No. 4.5e-20;  
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;  
  
QY 10 SSDLTWPAPKAGFY-AYLGVLVLLGLLNSIALWVFCRMOQWETRIYMTNLAVADLC 68  
Db 3 SSNCSTEDSFYKTLGXCVSMFVLGLIANCAVIAFTFLKVRNETTMYMLNLAISDL 62  
QY 69 LCLTLPFLVLSLRDSDTP---LQLSQGIYLTNRYMSISLVTAIADVRYAVVRPLRA 124  
Db 63 FVFTLPFRYIF-VVRNWFPGDVLCKVTLYFTYNNYGSILFTCLSDVRFLAIVHPFRS 121  
QY 125 RGLSPRQAAACAVLWLVLI-GSLVARWLLGIQEGGFCFST-RHNFNSMR-----FP- 176  
Db 122 KTLTKRNARIVCVAWITVLASTPASP-----FQSTNRQNTEQRTCFENPPE 171  
QY 177 -----LLGYPFLAVVVFCSLKVVTALAQRPPTDVGOABTRKAARMWA 221  
Db 172 STWKTYLSRIVIFIEIVGFIFLILNVCTSTWVLRTL-NKPLTLRNKLSKKKVLKMPV 230  
QY 222 NLLAVFVCPPLPHVGL---TVRLAVGNWACALLETIRRALYITSKLSDANCCLDAICYYY 278  
Db 231 HLIVFCFCVPYRNITILYSLMRTQTWNCVSVTAVRTVYPTVLCIAVSNCCFDPIVYF 290  
  
RESULT 13  
G09B\_HUMAN  
ID G09B\_HUMAN STANDARD; PRT; 387 AA.  
AC P49019;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Probable G protein-coupled receptor GPR109B (G protein-coupled receptor HM74).  
GN Name=GPR109B; Synonyms=HM74;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Monocytes;  
RX MEDLINE=94092629; PubMed=7505609;  
RA Nomura H., Nielsen B.W., Matsushima K.;  
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors.";  
RL Int. Immunol. 5:1239-1249(1993).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; D10923; BAA01721.1; -;  
DR PIR; I69202; I69202.  
DR HSSP; P34996; 1DDD.  
DR Genew; HGNC:16824; GPR109B.  
DR MIM; 606039; -;  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; TAS.  
DR InterPro; IPR000276; GPCR Rhodpsn.  
DR InterPro; IPR002286; P2\_purinocptor.  
DR Pfam; PF00001; 7tm1.1;  
DR PRINTS; PR00237; GPCRHHODOPS.  
DR PROSITE; PS00237; G-PROTEIN RECF\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECF\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane.  
FT DOMAIN 1 28 Extracellular (Potential).  
FT TRANSMEM 29 50 1 (Potential).  
FT DOMAIN 51 63 Cytoplasmic (Potential).  
FT TRANSMEM 64 85 2 (Potential).  
FT DOMAIN 86 102 Extracellular (Potential).  
FT TRANSMEM 103 123 3 (Potential).  
FT DOMAIN 124 142 Cytoplasmic (Potential).  
FT TRANSMEM 143 163 4 (Potential).  
FT DOMAIN 164 194 Extracellular (Potential).  
FT TRANSMEM 195 209 5 (Potential).  
FT DOMAIN 210 236 Cytoplasmic (Potential).  
FT TRANSMEM 237 256 6 (Potential).  
FT DOMAIN 257 273 Extracellular (Potential).  
FT TRANSMEM 274 298 7 (Potential).  
FT DOMAIN 299 387 Cytoplasmic (Potential).  
FT DISULFID 100 177 By similarity.  
SQ SEQUENCE 387 AA; 44481 MW; C244F562C2343647 CRC64;  
  
Query Match 22.8%; Score 368.5; DB 1; Length 387;  
Best Local Similarity 34.3%; Pred. No. 5.5e-20;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;  
  
QY 27 LGVLLVGLLNSIALWVFCRMOQWETRIYMTNLAVADLCCLTLPVL-----HSLR 81  
Db 34 LGLEFIFGLLGLNLWIFCFHLKSWKSRIFFNLAVADFLIITCLPFVMDYVYRRSDW 93  
QY 82 DTSDFPLCQLSQGIYLTNRYMSISLVTAIADVRYAVVRPLRARGLSRQAAAVCAVLW 141  
Db 94 NFGDIP-CLVLVFMFAMNRQSGIIFTVVADVRYFRVPHPHALNKISNWTAAISCLW 152  
QY 142 VLIVG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRPPLIGFYLPVLAVVVFCSLK 193  
Db 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICTFRWHEAMF-LLEFLPLGILLFCSAR 210  
QY 194 VVTLAQRPPTDVGOABTRKAARMWANLLVFVVCFLPLHVLGTLVRLAVGW-----N 246  
Db 211 IISLQR---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFMLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCLDAICYYYMAKEF 283  
Db 265 NCEYRSVDLAFITLSTFTYNNMLDPVVYIFSSPSF 301  
  
RESULT 14  
Q8NGE4  
ID Q8NGE4 PRELIMINARY; PRT; 387 AA.  
AC Q8NGE4;  
DT 01-OCT-2002 (TremBLrel. 22, Created)  
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
CC -----



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:17:30 ; Search time 19.5 Seconds  
(without alignments)  
1182.901 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGYNTCGSSDLTPPAIK.....AVAPRAKAKHSQDSLCTVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1609	99.6	309	3	US-09-422-869-20
2	401	24.8	370	3	US-08-781-250-2
3	374.5	23.2	387	4	US-09-170-496D-222
4	369.5	22.9	387	4	US-09-170-496D-108
5	369.5	22.9	387	4	US-09-944-807-21
6	360.5	22.3	344	2	US-08-467-948A-8
7	360.5	22.3	344	2	US-08-467-947A-8
8	359.5	22.3	302	2	US-08-467-948A-30
9	359.5	22.3	302	3	US-08-467-947A-30
10	328.5	20.3	377	4	US-09-745-842-17
11	327.5	20.3	374	4	US-09-102-710B-3
12	320	19.8	362	3	US-08-513-974B-374
13	318.5	19.7	346	4	US-09-585-876-2
14	317.5	19.7	391	4	US-09-826-509-463
15	316	19.6	374	4	US-09-745-842-15
16	315.5	19.5	365	4	US-09-745-842-16
17	315.5	19.5	365	4	US-09-077-173D-2
18	315	19.5	373	3	US-08-513-974B-373
19	311.5	19.3	354	4	US-09-364-425B-60
20	311.5	19.3	362	4	US-09-170-496D-4
21	311.5	19.3	364	4	US-08-148-708-2
22	310.5	19.2	358	4	US-09-170-496D-186
23	310	19.2	342	4	US-09-826-509-555
24	309	19.1	342	3	US-08-988-876-9
25	307.5	19.0	362	4	US-09-170-496D-166
26	306.5	19.0	375	1	US-08-442-134A-2
27	306.5	19.0	375	1	US-08-444-581B-2

28 306.5 19.0 375 1 US-08-446-088A-2 Sequence 2, Appli  
29 306.5 19.0 375 2 US-08-553-524A-3 Sequence 3, Appli  
30 306.5 19.0 375 3 US-08-749-707-3 Sequence 3, Appli  
31 306.5 19.0 375 4 US-09-947-922-3 Sequence 3, Appli  
32 305.5 18.9 327 3 US-08-513-974B-372 Sequence 372, App  
33 305.5 18.9 358 3 US-09-041-545-2 Sequence 2, Appli  
34 305.5 18.9 358 3 US-09-327-925-2 Sequence 2, Appli  
35 305 18.9 339 4 US-09-170-496D-182 Sequence 182, App  
36 303 18.8 342 4 US-09-054-272-2 Sequence 2, Appli  
37 302 18.7 326 1 US-08-118-270-39 Sequence 39, Appli  
38 302 18.7 326 5 PCT-US93-08528-39 Sequence 39, Appli  
39 301 18.6 328 3 US-08-513-974B-39 Sequence 39, Appli  
40 301 18.6 328 3 US-08-513-974B-371 Sequence 371, App  
41 301 18.6 328 4 US-09-461-436B-39 Sequence 39, Appli  
42 300.5 18.6 93 3 US-09-724-864-61 Sequence 61, Appli  
43 300.5 18.6 373 2 US-08-559-524A-4 Sequence 4, Appli  
44 300.5 18.6 373 3 US-08-749-707-4 Sequence 4, Appli  
45 300.5 18.6 373 4 US-09-947-922-4 Sequence 4, Appli

## ALIGNMENTS

RESULT 1  
US-09-422-869-20  
; Sequence 20, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SEENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG I.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-422-869-20

Query Match 99.6%; Score 1609; DB 3; Length 309;  
Best Local Similarity 99.7%; Pred No. 4.5e-132;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGYNTCGSSDLTPPAIKLGFYAYLGVLLVGLLLSLALWVFCRCMQQTETRIYMT 60  
Db 1 MNGYNTCGSSDLTPPAIKLGFYAYLGVLLVGLLLSLALWVFCRCMQQTETRIYMT 60  
QY 61 NLAVADLCLLCTLPVLHSLRDTSTPLCQLSQGIYLTNRNYSISLVTAIADRYAVVRH 120  
Db 61 NLAVADLCLLCTLPVLHSLRDTSTPLCQLSQGIYLTNRNYSISLVTAIADRYAVVRH 120  
QY 121 PLRAGLRSPQAAACAVLWLVLSVAVRWLLGIQGGGFCFTRNFNSMRPFLGCF 180  
Db 121 PLRAGLRSPQAAACAVLWLVLSVAVRWLLGIQGGGFCFTRNFNSMRPFLGCF 180  
QY 181 YLPLAVVFCSLKVVVTALAQRPTDVGQAEATRKAKRWANLLVYVVCFLFLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVVTALAQRPTDVGQAEATRKAKRWANLLVYVVCFLFLHVLTVR 240  
QY 241 LAVGNACALLETTRRALTYYITSKLSANDCLDIAICYWMAKEFQASALAVAPRAKHS 300







Db 234 HLIIFCFVFPYNILYSLVRTQTQFVNCVVAARVTWYPITLCLIAVSNCCFDPVIVYF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301  
RESULT 7  
US-08-467-947A-8  
; Sequence 8, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-947A-8  
Query Match 22.3%; Score 360.5; DB 3; Length 344;  
Best Local Similarity 29.2%; Pred. No. 1.2e-23;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFIAYL-GVLLVLGLLNSLALWFCRCMQQWETRIYMTNLAVADLC 68  
Db 6 SSHCFYNDSEFKYTLGCMFSWVFLGLNSLALWFCRCMQQWETRIYMTNLAMSDLL 65  
QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDYVAVRHPLRA 124  
Db 66 FVFTLPFRIFYP-TTRNWFPGDLLCKISWMLFTYNNYGSILFLTCISVDRFLAIVYPPKS 124  
QY 125 RGLRSQRAAAVCAVLWLVI-GSLVARWLLGIQEGG-----FCFRSTRHNFSMRFP-- 176  
Db 125 KTI:RTKRNAKIVCTGWLTAVIGSGAPAVFQVQTHSQGNNAEACFEN-----FPBA 175

QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVQGAETR-KAKRMVWA 221  
Db 176 TWKYVLSRIVFIEIVGFIFLILNVTCTSSWVLKTLTK--PVTLSRSKINKTKVLKMFV 233  
QY 222 NLLVFWCFLPLHVLGTLVRLAVGNA----CALLETIRALYITSKLSDANCCLDICYY 278  
Db 234 HLIIFCFVFPYNILYSLVRTQTQFVNCVVAARVTWYPITLCLIAVSNCCFDPVIVYF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301  
RESULT 8  
US-08-467-948A-30  
; Sequence 30, Application US/08467948A  
; Patent No. 5998164  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR2  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,948A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-467-948A-30  
Query Match 22.3%; Score 359.5; DB 2; Length 302;  
Best Local Similarity 30.0%; Pred. No. 1.3e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFIAYLGVLLVLGLLNSLALWFCRCMQQWETRIYMTNLAVADLC 68  
Db 1 SENCSTEDSEFKYTLGCVFSWVFLGLNCAVIAIYFTFLKVRNETTYTMLAISDLL 60  
QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYMSISLVTAIAVDYVAVRHPLRA 124

Db 61 FVFTLPERIYF-VVRNMPFGDLCKISVTLFTYTNMGYSILFLTCISVDRFLAIVHPERS 119  
QY 125 RGLRSPROAAVCAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----PP- 176  
Db 120 KTLRTKRNARIVCAVAVITVLGSPASF-----FQSTNRQNNTEQRTCPENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVGOAEATRKAKRWYWA 221  
Db 170 STWKTYLSRIVIFIBIVGFPIILINVTCTWLVRTL-NKPLTLSRNKLKSKKVKLMFV 228  
QY 222 NLLVFWVCFPLHVLG1---TVRLAVGWNACALLETIRRALYITSKLSANCCCLDAICY 278  
Db 229 HLVIFFCFVFNITLILYSLMRTQWNCVVTAVRTMYPVTLCLAVSNCCFDPVIVYF 288

## RESULT 9

US-08-467-947A-30  
; Sequence 30, Application US/08467947A  
; Patent No. 6090575

## GENERAL INFORMATION:

; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

## COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/467,947A

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/04079

; FILING DATE: 30-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 302 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-08-467-947A-30

Query Match 22.3%; Score 359.5; DB 3; Length 302;

Best Local Similarity 30.0%; Pred. No. 1.3e-23;

Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;

QY 10 SSDLTWPAIKLGFY-AVLGVLVLLGLLNSLALWVFCRCMQQWTEIRYTNLAVADLC 68

Db 1 SNNCTSDSFKTYLIGCVFWMVFLGLIANCAVIAIYFTFLKVRNETTTMLMLAISDLL 60

QY 69 LLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSISLVTALAVDRYVAVRHLRA 124  
Db 61 FVFTLPERIYF-VVRNMPFGDLCKISVTLFTYTNMGYSILFLTCISVDRFLAIVHPERS 119  
QY 125 RGLRSPROAAVCAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----PP- 176  
Db 120 KTLRTKRNARIVCAVAVITVLGSPASF-----FQSTNRQNNTEQRTCPENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVGOAEATRKAKRWYWA 221  
Db 170 STWKTYLSRIVIFIBIVGFPIILINVTCTWLVRTL-NKPLTLSRNKLKSKKVKLMFV 228  
QY 222 NLLVFWVCFPLHVLG1---TVRLAVGWNACALLETIRRALYITSKLSANCCCLDAICY 278  
Db 229 HLVIFFCFVFNITLILYSLMRTQWNCVVTAVRTMYPVTLCLAVSNCCFDPVIVYF 288

## RESULT 10

US-09-745-842-17

; Sequence 17, Application US/09745842

; Patent No. 6762029

; GENERAL INFORMATION:

; APPLICANT: Conley, Pamela B.

; APPLICANT: Jantzen, Hans-Michael

; APPLICANT: Ramakrishnan-DuBridge, Vanitha

; APPLICANT: Julius, David

; APPLICANT: Hollopeter, Gunter

; APPLICANT: COR Therapeutics, Inc.

; TITLE OF INVENTION: P2Y12 Receptor

; FILE REFERENCE: 44481-5053-US

; CURRENT APPLICATION NUMBER: US/09/745,842

; CURRENT FILING DATE: 2000-12-26

; PRIOR APPLICATION NUMBER: US 60/171,622

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 377

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur

US-09-745-842-17

Query Match 20.3%; Score 328.5; DB 4; Length 377;

Best Local Similarity 33.1%; Pred. No. 7.8e-21;

Matches 90; Conservative 47; Mismatches 108; Indels 27; Gaps 8;

QY 28 GVLVLGLLNSLALWVFCRCMQQWTEIRYTNLAVADLCCLTLPFVLHSLRDTSDTP 87

Db 41 GWVCVLGLCLNAVALYIFLCRLKTNWASTTYMFHLAVSDALYAAASLPLLVYYYARGDHP 100

QY 88 ---LCQLSQGIYLTNRYSISLVTALAVDRYVAVRHLRARGLSRQAAAACAVLWVL 143

Db 101 FSTVLCKLVRFLFYTNLYCSILFLTCISVHRCGLVRLRSURWGRYARRVAGAVWL 160

QY 144 VIG--SLVARWLLG1QEGGFCFRSTRN-----FNSMRFPFLGFLPLAVVYF 189

Db 161 VLACQAPVLYFVTTTSARG--RVTCHDTSAPELFSRFVAYSSVLMGLL-FAVPFAVILV 216

QY 190 CSLKVVVTALAQRP--TDVGQAEATRKAKRWYWANLLVFWVCFPLHVLGTLVRLAVGM-- 245

Db 217 CAVLMARLL-KPAYGTSGGLPRAKRKSVRTIAVLAVALCFLPFPHVTRTLTYSPRSID 275

QY 246 NACALLETIRRALYITSKLSANCCCLDAICY 277

Db 276 LSCHTLNAINWAYKVTRPLASANSCLDPVLYF 307

## RESULT 11

US-09-102-710B-3

; Sequence 3, Application US/09102710B

; Patent No. 6479630

```
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: RNU09402
US-09-102-710B-3

Query Match      20.3%; Score 327.5; DB 4; Length 374;
Best Local Similarity 29.2%; Pred. No. 9.4e-21;
Matches 99; Conservative 54; Mismatches 127; Indels 59; Gaps 10;

QY 2 NGTYNTCGSSDLTWPPAIIKLG- - - - -YAYL- - - - -GVLLVGLLNSLALWVFCR 48
DB 9 NSTINGTWGD- - - - -ELGKCRNEDFKYVLPVSGVGVVGLCLNVVALYFLCR 61

QY 49 MOQWETRIYMTNLAVADCLCTLPFVLHSLRDTSDTP- - - - -LCQLSQGIYLTNRYMSI 104
DB 62 LKTNASTTYMFLHVASDSLAAASLPLLYVYAQGDHWPFTVLCVLFVFTNLYCSI 121

QY 105 SILTAIVDRYVAVRHPLRAGRLSPROAAACAVLWLVIGS- - - - -LVARWLLIGQE 158
DB 122 LFLTCISVHSLGVLRLPLSLRWGHARYARRVAAVWVVLVACQTPVLYFVFTTSVRGT- - 179

QY 159 GGFGRSTRHN- - - - -FNSMRPFLGFLPLAVVYVFCSLKVVTALAQRPPTDV 206
DB 180 - - - - -RITCHDTSDELFSHFVAYSSVMGLL-FAVPSIILVYVMARLLKPAYGTT 233

QY 207 GOAEATRKAKRMVWNLVYVVCFLPLHVLGLTVRLAVGW- - - - -NACALLETIRRALYITSKL 264
DB 234 GLPRAKRSVRTIALVLAVFALCFPLPFHVTRTLVYFSRLDLSCHTLNAINMAYKITRPL 293

QY 265 SPANCLDAICYY- - - - -MAKEQOEASALAVAPRAK 296
DB 294 ASANSCLDPVLYFLAQRLVRFARDAKPATEPTPSQAR 332

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: D'KE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-374

Query Match      19.8%; Score 320; DB 3; Length 362;
Best Local Similarity 28.2%; Pred. No. 4.1e-20;
Matches 96; Conservative 64; Mismatches 133; Indels 48; Gaps 12;

QY 1 MNGTY- - - - -NTCGSSDLTWPPAIIKLG- - - - -YAYLGVLLV- - - - -GLLNSLALWV 44
DB 10 LMGTPPELLAGGWAAGNATTKCSLT- - - - -KTGFQFYLPVTVVILVITGFLGNSVAIWM 64

QY 45 FCRMQQWETRIYMTNLAVADCLCTLPFVLHSLRDTSD- - - - -TPLCQLSQGIYLTNR 100
DB 65 FVFHMRPMSGISVYTMFNALADFLVYLTLPALIFYFYFNKTDWIFGDMCKLQRFIFHVN 124

QY 101 YMSISLVTAIVDRYVAVRHPLRAGRLSPROAAACAVLWLVIGSLVARWL- - - - -LGI 156
DB 125 YGSILFLTCISVHRYTGVVHPLKSLGRKKKNAVYVSSLVWALV- - - - -AVTAPILFYSGIGV 183

QY 157 QEGG- - - - -FCFRSTRHNF- - - - -NSMRPFLGFLPLAVVYVFCSLKVVTALAQRPPTDVQ 208
DB 184 RRNKTITCYDTTADAYLRSYFVYSMTCTVFMFCIPFVILGCVGLIVKALIK- - - - -DLDN 240
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:25:32 ; Search time 55 Seconds  
(without alignments)  
1879.324 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGYNTCGSSDLTWPPAIPK.....AVAPRAKHKQDSLCTVTLA 309

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609	99.6	309	9	US-09-768-877-20
2	1609	99.6	309	14	US-10-225-567A-492
3	1609	99.6	309	17	US-10-696-639-44
4	1597	98.9	309	14	US-10-157-031-351
5	401	24.8	370	10	US-09-964-821B-11
6	401	24.8	370	14	US-10-081-810-44
7	401	24.8	370	14	US-10-225-567A-225
8	401	24.8	370	14	US-10-024-298A-176
9	401	24.8	370	14	US-10-042-211A-176
10	401	24.8	370	14	US-10-268-332-11
11	401	24.8	370	15	US-10-617-217A-176
12	401	24.8	370	17	US-10-753-267-86
13	400	24.8	370	10	US-09-964-821B-10

14	400	24.8	370	14	US-10-268-332-10
15	391	24.2	370	14	US-10-024-298A-174
16	391	24.2	370	14	US-10-042-211A-174
17	391	24.2	370	15	US-10-617-217A-174
18	382.5	23.7	363	16	US-10-314-048A-159
19	382.5	23.7	363	16	US-10-897-815-159
20	377.5	23.4	363	10	US-09-930-334-16
21	377.5	23.4	363	15	US-10-619-141-16
22	376.5	23.3	363	14	US-10-321-807-36
23	376.5	23.3	363	15	US-10-295-027-226
24	376.5	23.3	363	15	US-10-292-798-668
25	376.5	23.3	363	16	US-10-321-807-36
26	376.5	23.3	363	16	US-10-314-048A-36
27	376.5	23.3	363	16	US-10-897-815-36
28	376.5	23.3	364	14	US-10-017-161-766
29	376.5	23.3	382	14	US-10-017-161-808
30	374.5	23.2	387	14	US-10-251-385-222
31	374	23.2	319	14	US-10-167-192-1
32	374	23.2	319	15	US-10-400-991-4
33	372.5	23.1	387	10	US-09-930-334-2
34	372.5	23.1	387	15	US-10-619-141-2
35	369.5	22.9	339	14	US-10-188-149A-4
36	369.5	22.9	387	9	US-09-944-807-21
37	369.5	22.9	387	14	US-10-092-135-8
38	369.5	22.9	387	14	US-10-251-385-108
39	369.5	22.9	387	14	US-10-240-842-4
40	369.5	22.9	387	14	US-10-225-567A-281
41	369.5	22.9	387	14	US-10-296-223-4
42	369.5	22.9	387	14	US-10-348-083-3
43	369.5	22.9	387	14	US-10-044-643-43
44	369.5	22.9	387	15	US-10-295-027-224
45	369.5	22.9	387	15	US-10-295-027-228

#### ALIGNMENTS

#### RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/768,877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422,869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-768-877-20

Query Match 99.6%; Score 1609; DB 9; Length 309;  
Best Local Similarity 99.7%; Pred. No. 5.3e-147;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNGYNTCGSSDLTWPPAIPKLGFGVAYLGLVLLGLNLSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGYNTCGSSDLTWPPAIPKLGFGVAYLGLVLLGLNLSLALWVFCRCMQQTETRIYMT 60





Query Match 98.9%; Score 1597; DB 14; Length 309;  
Best Local Similarity 99.0%; Pred. No. 7.6e-146;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIGFYAYLGVLVGLLLNSLALWVFCRMOQWTEIRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPPAIGFYAYLGVLVGLLLNSLALWVFCRMOQWTEIRIYMT 60

QY 61 NLAVADCLLCTLPVLHSLRSDTSLCQISQGIYLTNRNYSISLVTAIADVAVRH 120  
DB 61 NLAVADCLLCTLPVLHSLRSDTSLCQISQGIYLTNRNYSISLVTAIADVAVRH 120

QY 121 PLRARGLSRPROAAVCAVLVWLVGSLVAPWLLGQSGFCFRSTRNFNSMRPFLG 180  
DB 121 PLRARGLSRPROAAVCAVLVWLVGSLVAPWLLGQSGFCFRSTRNFNSMRPFLG 180

QY 181 YPLAVVVFCSLKVVYTAQRPPTDVGQAEATRKARWVANLLVFWVCFPLHVLTVR 240  
DB 181 YPLAVVVFCSLKVVYTAQRPPTDVGQAEATRKARWVANLLVFWVCFPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLCTVLA 309  
DB 301 QDSLCTVLA 309

RESULT 5  
US-09-964-821B-11  
; Sequence 11, Application US/09964821B  
; Publication No. US20030186360A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M. G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3,  
; FILE REFERENCE: D0042NP  
; CURRENT APPLICATION NUMBER: US/09/964,821B  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,783  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-821B-11

Query Match 24.8%; Score 401; DB 10; Length 370;  
Best Local Similarity 34.1%; Pred. No. 3.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVGLLVGLLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQISQGIYLTNRNYSISLVTAIADVAVRHPLRARGLSRPROAAVCAVL 140  
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPPRSRTIRNRNSAIVCAGV 162

QY 141 WLVITGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLIGFYPLAVVVF 189  
DB 163 WILVLSGGISASLFTSTTNVNNATTTTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLILNS 222

QY 190 CSLKVVYTAQRPPTDVGQAEAT-RKAKRWVANLLVFWVCFPLHVLTVRLAVGNAC 248  
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFCVPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKSODSLC 305  
DB 281 TNCFLERFAKIMYPITLCLATLNCDFPIYYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307  
DB 335 KT 336

RESULT 6  
US-10-081-810-44  
; Sequence 44, Application US/10081810  
; Publication No. US20030064438A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI  
; FILE REFERENCE: D0132 NP  
; CURRENT APPLICATION NUMBER: US/10/081,810  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: US 60/270,793  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/270,792  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/296,427  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-081-810-44

Query Match 24.8%; Score 401; DB 14; Length 370;  
Best Local Similarity 34.1%; Pred. No. 3.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVGLLVGLLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQISQGIYLTNRNYSISLVTAIADVAVRHPLRARGLSRPROAAVCAVL 140  
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPPRSRTIRNRNSAIVCAGV 162

QY 141 WLVITGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLIGFYPLAVVVF 189  
DB 163 WILVLSGGISASLFTSTTNVNNATTTTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLILNS 222

QY 190 CSLKVVYTAQRPPTDVGQAEAT-RKAKRWVANLLVFWVCFPLHVLTVRLAVGNAC 248  
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFCVPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKSODSLC 305  
DB 281 TNCFLERFAKIMYPITLCLATLNCDFPIYYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307  
DB 335 KT 336

RESULT 7

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; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.8%; Score 401; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLGVLLVGLLINSLSLAWFCRCMQQWETRIYMTNLSLAVADICLLCTLP-VLHSLR-- 81
DB      44  AVSVVFIIGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNRHR 103

QY      82  -DTSDDPLQCLSGIYLTNRYMSISLVTALVDYVAVRHLRARGLSRQAAAVCAVL 140
DB      104  WPGEDT-LCKISGTAFLTNYGSMFLTCLISVDRLAIVYFPRSRTTTRNSAIVCAGV 162

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHFNMSR--FPLLGYPPLAVVVF 189
DB      163  WILVLSGGISASLFTSTNVNNAITTCFEGFSKRVWKYLSKITFIIEVGVFIILNLVS 222

QY      190  CSLKVVYTAQRPPTDVQAEAT-RKAKRMVWANLLVYVVCFLPHVGLTVRLAVGWNAC 248
DB      223  CSSWVLRTL--RKPAFLSQITGNKKVLYKMITVHMAVFVVCVPYNSVLFLYALVRSOAI 280

QY      249  --ALLTIRRALY-ITSKLSDANCCLDAICYYYMAKEFQBASALAVAPRAKAHKSQDSL 305
DB      281  TNCFLERPAKIMYPITLCIATLNCPPFIYFTLESFQSKFYI-----NAHIRMESLP 334

QY      306  VT 307
DB      335  KT 336

RESULT 9
US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFKB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.8%; Score 401; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.2e-30;

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Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVYGVLLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIADRVAVVHPLRARGLSRPRQAAVCAVL 140
Db 104 WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPPRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARLLGQIE-----GGFCFRSTRHNFNSMR--FPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVVTAQAORPPTDVGOAEAT-RKAKRMVWVANLLVFCVCLPLHVLGTLVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPAATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 10
US-10-268-332-11
; Sequence 11, Application US/10268332
; Publication No. US20030175748A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM3, EXPRESSED HIGHLY
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-11

Query Match 24.8%; Score 401; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVYGVLLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIADRVAVVHPLRARGLSRPRQAAVCAVL 140
Db 104 WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPPRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARLLGQIE-----GGFCFRSTRHNFNSMR--FPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVVTAQAORPPTDVGOAEAT-RKAKRMVWVANLLVFCVCLPLHVLGTLVRLAVGWNAC 248
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RESULT 12

US-10-753-267-86

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Db 223 CSSVVLRTL--RKPAATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 11
US-10-617-217A-176
; Sequence 176, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176

Query Match 24.8%; Score 401; DB 15; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVYGVLLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIADRVAVVHPLRARGLSRPRQAAVCAVL 140
Db 104 WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPPRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARLLGQIE-----GGFCFRSTRHNFNSMR--FPLLGFLYPLAVVVF 189
Db 163 WILVLSGGISASLFTSTNNVNNATTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVVTAQAORPPTDVGOAEAT-RKAKRMVWVANLLVFCVCLPLHVLGTLVRLAVGWNAC 248
Db 223 CSSVVLRTL--RKPAATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 12
US-10-753-267-86
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; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP008912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 174  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
  
US-10-024-298A-174
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Query Match            24.2%; Score 391; DB 14; Length 370;  
Best Local Similarity 34.5%; Pred. No. 2.9e-29;  
Matches         97; Conservative 58; Mismatches 104; Indels 22; Gaps 9;

	Qy	25	A Y L G V L I V L G L L N S A L W F C R M Q O W T E T R I Y M N L A V D I C L L C T I P F - V L H S L R -- 81
	Dd	44	A V S V V F I L G I T N S A S L F V C F C P K M R S E T A T F I T N L A S L D L L F V C T L P F K Y F N F R H 103
	Qy	82	-DTS-DTPLCOLSQGVILTNRYMISLIVTAIDRVYAVVRHPLRARGLRSPROAAVCAVL 140
	Dd	104	WPFGDT-LCKISTGFELNLYGSMLFCLCSVDRFALIAVVYPFSRTITRNSAIUCAGV 162
	Qy	141	VWLVIQSGLVARLLGIQE-----GGFCFRSTRHNFNMSMR--FPFLFGYLPLAVVFV 189
	Dd	163	WI LVSGGISASLFSTNNVNATTCTCEFGSKRWKTYLSKITIFIEVGWFIIPLLNVS 222
	Qy	190	CSLKVTALTAAQRPTDVGOAEAT-RKA RKMVMWANLVFVVCFEPLHVGLTVRLAVGNAC 248
	Dd	223	CSSVWRLT---RKPA TSIGTGKKVKLMITVHMVAFFVCVPFYNSVLFIAYLRSOAI 280
	Qy	249	--ALLETIRRALY-ITSKLSDANCCLD AICYYYMAKEFOEA 286
	Dd	281	TNCLEERFAKIWPITLCLATINCCPDPPIYYFTLBESFKS 321

Search completed: May 23, 2005, 11:33:03  
Job time : 56 secs

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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:15:00 ; Search time 17 Seconds  
(without alignments)  
1748.881 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTWPPAIAK.....AVAPRAKHSQDSLVCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	400	24.8		370	2	JC5549	heptahelical P2Y5-
2	369.5	22.9		387	2	I69202	G protein-coupled
3	367.5	22.8		308	2	I50241	G protein-coupled
4	359.5	22.3		344	2	T09508	intron 17 purinerg
5	317	19.6		373	2	A47556	ATP receptor P2u -
6	316	19.6		362	2	S33733	G protein-coupled
7	315.5	19.5		365	2	S68679	G protein-coupled
8	314	19.4		328	2	I5450	G protein-coupled
9	311.5	19.3		354	2	I53033	G protein-coupled
10	311.5	19.3		362	2	A57641	G protein-coupled
11	311.5	19.3		364	2	J01488	bradykinin B2 rece
12	311.5	19.3		366	1	O0RTB2	bradykinin recepto
13	309	19.1		342	2	S13638	platelet-activatin
14	308.5	19.1		362	2	B57641	G protein-coupled
15	307.5	19.0		362	2	S68207	G protein-coupled
16	306.5	19.0		375	2	A54946	P-2U nucleotide re
17	303	18.8		342	2	A40191	platelet-activatin
18	303	18.8		352	2	S60024	angiotensin II rec
19	300.5	18.6		373	2	J04162	chemokine (C-C) re
20	296.5	18.4		373	2	J04737	p2Y receptor - bov
21	292	18.1		341	2	S43252	G protein-coupled
22	288	17.8		363	2	J02543	platelet-activatin
23	286.5	17.7		352	2	A43113	angiotensin II rec
24	286	17.7		328	2	J04800	p2Y6 receptor - hu
25	284.5	17.6		361	2	B45680	G protein-coupled
26	282	17.5		341	2	S63666	platelet-activatin
27	280.5	17.4		366	2	I49519	bradykinin B2 rece
28	279.5	17.3		361	2	J05653	G protein-coupled
29	278.5	17.2		363	2	I57955	somatostatin recep

RESULT 1

JC5549  
heptahelical P2Y5-like receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5549  
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.  
Biochem. Biophys. Res. Commun. 236, 106-112, 1997  
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.  
A:Reference number: JC5549; MUID:97366605; PMID:9223435  
A:Accession: JC5549  
A:Molecule type: DNA  
A:Residues: 1-370 <JAN>  
C:Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2  
C:Superfamily: ATP receptor P2u

Query Match 24.8%; Score 400; DB 2; Length 370;  
Best Local Similarity 34.0%; Pred. No. 1.8e-29;  
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

Qy	25	AYLVGLVLLGLLNSLALWVFCBMOQWTEIRIVMTNLAVADLCCLCTLPF-VLHSLR--	81
Db	44	AVYSVWFILGUITNSVLSLVFCFRMKRSETAIFITNLAVSDLLFVCTLPKIFNFNRH	103
Qy	82	-DTSPTPLCOLSQGIIYLTNRYMSISLTAIAVDYVAVRHPLRGLRSPQAAACAVL	140
Db	104	WPFQGT-LCKISGTAFLTNIGSMLFLTCISVDRFLAIVYFRSRTITRNSAIVCAGV	162
Qy	141	WVLVIGSLVARWLLGIOEGGF-----CFR-----STRHFNNSMRFPILLGPVL	182
Db	163	WILVLSG-----GISASLFTTNVNNATTTCFGLSKRWKTYLSKITIFIEVVGPII	215
Qy	183	PLAVVFCSLKVVTALQRPPTDVQAEAT-RKAKRMVWVWNLVYVVCFLPLHVLGTVRL	241
Db	216	PLILNVSCSSVVLRTL--RKEATLSQIGTNKKVLMKMTVMHMAVFWVFCVYNSVLFYLA	273
Qy	242	AVGNWAC--ALLETIRALY-ITSKLSDANCLDAICYVMYMAKFEQESALAVAPRAKAH	298
Db	274	LVRQAIQTNCFLEFAKIMYFITCLATLNCDFPIFYFTLESFQKSFYI-----NAH	327
Qy	299	KSQDSLQCVT 307	
Db	328	IRMESLFKT 336	

RESULT 2

I69202  
G protein-coupled receptor HM74 - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I69202  
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

F;269-292/Domain: transmembrane #status predicted <TM7>

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Query Match      22.8%; Score 367.5; DB 2; Length 308;
Best Local Similarity 30.3%; Pred. NO. 1.ee-26;
Matches          91; Conservative    64; Mismatches   102; Indels    43; Gaps     10;
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QY    10 SSDLTWPPAAIKLGFY-AYLGVLLVLGLLNLSALWVFCRCCMOOWTETRIYMTNLAVADLC 68  
       || : : | : | : | : | : | : | : | : | : | : | : | : | :  
Db      3 SNNCSDESKFITYLGCVSMVFGLIANCAVIYFTFLKVRNNTTYMLNALISDLL 62

Db	63	FVFTLPRYYYF-VWRNPFEGDVLCKISVTLFTFNMYGSLFTCTISVDPLALVHPFRS	121
QY	125	RGLSRQRAAAVCAVLWLVI-GSLVARMLLGIQEGGFCFRST-RHNFNSMR-----FP-	176
Db	122	KLTLTKRNARIVCAVWITVLASTPASP-----FQSTRQNNTQRTCFENFPE	171
QY	177	-----LLGYLPLAVVVFCSKLVVTTALAAQRPPTDVGQAEATRKAIRMVWA	221
Db	172	STWKTYLSRIVIFIEIVGFIPILLNVCTSMVLTLL-NKPLTLSRNLKSKVKVLMIFV	230
QY	222	NLAVFVVCFLPLHVLG---TVRLAVGNACALLETIRRALYITSKUSDANCCCLDAICYYY	278
Db	231	HLVIFCFCEFPVNTILYLSLMTOTWINGSVVTAVRTWYPTVLTCLIAVSNCCFPEIYYF	290

A;Reference number: Z16705

[illegible]



Db 294 TSDITIONS 301

RESULT 5

A47556

ATP receptor P2u - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: A47556

R:Jushtig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A:Reference number: A47556; MUID:93281707; PMID:7685114

A:Accession: A47556

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-373 <US>

A:Cross-references: UNIPROT:P35383; GB:L14751; NID:G309457; PIDN:AAA39871.1; PID:G309458

C:Superfamily: ATP receptor P2u

C:Keywords: transmembrane protein

Query Match 19.6%; Score 317; DB 2; Length 373;

Best Local Similarity 30.1%; Pred. No. 9.2e-22;

Matches 101; Conservative 54; Mismatches 130; Indels 50; Gaps 11;

QY 2 NGTYNTCGSSDLTWPAPKLG- - - - -YAYL- - - - -GVLLVLGLLNSLALWVFCR 48

Db 9 NSTINGWEGD- - - - -ELGKCRFNEDEKVVLLPVSGVGVVCLGLNVALVFLCR 61

QY 49 MQOWTETRIYMTNLAVADCLLCTLPFVLHSLRDTSDTP- - - - -LCQLSQGYLTNRYSI 104

Db 62 LKTNWASTYMPHLAVSDSLYAAASLPLVYVYARGDHPFSTVLCVLRFLFYTNLYCSI 121

QY 105 SLVTAIAVDVRYVAVRHPLRARGLRSPROAAACAVLWLVIGSLVARWLLGQEGGFCPR 164

Db 122 LFLTCISVHRCLGVLRPLHSLRWGRYARVAAVWVLLV-ACQAPVLYFTTTSVRGTR 180

QY 165 STRHN- - - - -FNSMRFPILLGFYPLVAVVFCVSLKVVVTAQAQPP- - - - -TDVGQAE 210

Db 181 ITCHDTSARELPSHFVSSVMGLL-FAVPSVILVCVLMARLL-KPAYGTTGGLPR 238

QY 211 ATRKAKRMWVANLLVFFVFCVPLHVLTVRLAVGH- - - - -NACALLETIRRALYITSKLSDAN 268

Db 239 AKRKSVRTIALVAVFALCFPHFVTRTYLTSFRSLDLSCHTLNINWAYKITRPLASAN 298

QY 269 CCLDAICYYY- - - - -MAKEFQEAALAVAPRAK 296

Db 299 SCLDPVLYFLAGQRLVRFARDAKPTEPTSPQAR 333

RESULT 6

S33733

G protein-coupled receptor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S33733

R:Webb, T.E.; Simon, J.; Krishan, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock

FEBS Lett. 324, 219-225, 1993

A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A:Reference number: S33733; MUID:93285340; PMID:8508924

A:Accession: S33733

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-362 <WEB>

A:Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CAA51716.1; PID:G39509

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.6%; Score 316; DB 2; Length 362;

Best Local Similarity 28.2%; Pred. No. 1.1e-21;

Matches 96; Conservative 63; Mismatches 134; Indels 48; Gaps 12;

QY 1 MNGTY- - - - -NTCGSSDLTWPAPKLG- - - - -YAYLGVLLVL- - - - -GLLNSLALWV 44

Db 10 LNGTOPELLAGCGAAGNATTKCSLT- - - - -KTGFQFYLLPTVYILVFFITGFLGNSVAIHM 64

QY 45 FCCRMQOWTETRIYMTNLAVADCLLCTLPFVLHSLRDTSD- - - - -TPLCOLSQGYLYTNR 100

Db 65 FVFHMRPWSGISVYMFNLALADFLVLTLPALIFYFNKTDWIFGDVCKLQRFIFHVL 124

QY 101 YMSISLVTAIAVDVRYVAVRHPLRARGLRSPROAAACAVLWLVIGSLVARWLL- - - - -GI 156

Db 125 YGSILFLTCISVHRYTGVVHPPLKSLGRLLKKNVAVVSSLVWALV- - - - -AVIAPILFYSGTG 183

QY 157 QEGG- - - - -FCFRSTRHNF- - - - -NSMRFPILGFLYPLAVVFCVSLKVVVTAQAQPPDVCQ 208

Db 184 RNNKITCYDTTADSEYLSRYFVYSMCTTVFMECIPFVILGCGYGLVIALIYK- - - - -DLON 240

QY 209 AEATRKAKRMWVANLLVFFVFCVPLHVLTVRLAVGWN- - - - -ACALLETIRRALYITSK 263

Db 241 SPLRKSIVLVIIVLTVPFVAVSLPHVMKLTNLRARLDFQTPQMCANFKVATYQVTRG 300

QY 264 LSDANCCLDATCYNYMAKEFQEAALAVAPRAKAKHSQDSL 304

Db 301 LASLNSCVDPIYFLAGDTFRR- - - - -RLSRATRKSSRRSEPNV 339

RESULT 7

S68679

G protein-coupled receptor - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S68679

R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.

FEBS Lett. 384, 260-264, 1996

A:Title: Molecular cloning and characterization of a novel orphan receptor (p(2P)) expr:

A:Reference number: S68679; MUID:96197801; PMID:8617367

A:Accession: S68679

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STA>

A:Cross-references: UNIPROT:P51582; EMBL:X96597; NID:G1296631; PIDN:CAA65415.1; PID:G1296631

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor

Query Match 19.5%; Score 315.5; DB 2; Length 365;

Best Local Similarity 29.2%; Pred. No. 1.2e-21;

Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

QY 29 VLLVLGLLNSLALWVFCRQOWTETRIYMTNLAVADCLLCTLPFVLHSLRDTSDTP- 87

Db 44 VVFLGLGLNAPTLWLFIRLRPMDATATYMPHLASDLYVLSLPTLIYYAAHNHWP 103

QY 88 - - - - -LCQLSQGYLYTNRYSISLVTAIAVDVRYVAVRHPLRARGLRSPROAAACAVLWLV 144

Db 104 GTEICKFVRFLFYWNLYCSVFLTCISVHRYLGICHPRLARLWGRPRLAGLCLAVLV 163

QY 145 IGSILVAR- - - - -WLLIQEGG- - - - -FCFRSTR- - - - -H- - - - -NFSMRFPILGFLYPLAVVFCVSLK 193

Db 164 AGCLVPNLFVFTTSNKGTTVLCHDTRPEEPDHYVHFSSAVMGLL- - - - -FGVPCLVLTVCYGL 222

QY 194 VVTAQAQPPDVGQAEATRAK- - - - -RMVWVANLLVFFVFCVPLHVLTV- - - - -RLAVGWNA 247

Db 223 MARRLYQPLP- - - - -GSAQSSRLRSRTTAVVLTFAVCFVPPPHITTYTLARLLEA- - - - -D 277

QY 248 CALLETIRRALYITSKLSDANCCLDATCYNYMAKEFQEA- - - - -ASALAV 291

Db 278 CRVLNIVNVVYKTRPLASNSCLDPVLYLLTGDKYRRLQRLCGGKPPQPTAASSIAL 337

QY 292 APRAK- - - - -AHKSQDSLCVT 307

Db 338 VSLPEDSSCRWAATPDSSCST 359

RESULT 8



A:Reference number: JH0712; MUID:93038601; PMID:1329734  
A:Accession: JH0712  
A:Molecule type: DNA  
A:Residues: 1-364 <EGG>  
A:Cross-references: UNIPROT:P30411; GB:S45489; NID:g256536; PIDN:AAB23467.1; PID:g256537  
R:Powell, S.J.; Slyn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.  
Genomics 15, 435-438, 1993  
A:Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to chromosome 15  
A:Reference number: A46022; MUID:93194199; PMID:7916737  
A:Accession: A46022  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-364 <POW>  
A:Cross-references: GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:g298605  
A:Note: sequence extracted from NCBI Backbone (NCBIN:127280, NCBI:P:127284)  
R:Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.  
Genomics 23, 362-369, 1994  
A:Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human bradykinin receptor type B2  
A:Reference number: A55559; MUID:95137582; PMID:7835885  
A:Accession: A55559  
A:Molecule type: DNA  
A:Residues: 1-364 <MAA>  
A:Cross-references: GB:L27594  
R:Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.  
Biochem. Biophys. Res. Commun. 184, 260-268, 1992  
A:Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor  
A:Reference number: JQ1488; MUID:92231936; PMID:1314587  
A:Accession: JQ1488  
A:Molecule type: mRNA  
A:Residues: 1-364 <HES>  
A:Cross-references: GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:g1388000  
C:Genetics:  
A:Gene: GDB:BDKRB2  
A:Cross-references: GDB:L35713; OMIM:113503  
A:Map position: 14q32.1-14q32.2  
A:Map position: 14q32.1-14q32.2  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F:34-56/Domain: transmembrane #status predicted <TM1>  
F:66-92/Domain: transmembrane #status predicted <TM2>  
F:104-127/Domain: transmembrane #status predicted <TM3>  
F:148-171/Domain: transmembrane #status predicted <TM4>  
F:195-221/Domain: transmembrane #status predicted <TM5>  
F:241-266/Domain: transmembrane #status predicted <TM6>  
F:285-309/Domain: transmembrane #status predicted <TM7>  
F:312-180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:170,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F:242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F:316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.3%; Score 311.5; DB 2; Length 364;  
Best Local Similarity 27.6%; Pred. No. 2.9e-21;  
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;  
Qy 1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGVLLVGLLNSLALVVFCCRMQOW 52  
Db 11 LNGTFAQSKQVWGLWLTQPP-----FLWLVFLVLTLENIFLVSVFCLHKSSC 62  
Qy 53 TETRIYMTNLAVADICLLCTLPVLSLRDTS-----TPLCQLSQGIYLTNRYSISLVT 108  
Db 63 TVAEIYLGNTAAADLIACGLFPFWAITISNFDWLFQSTLCRVVNAIISNNLYSSICFLM 122  
Qy 109 AIAVDYVAVRPLRARGLRSPROAAVCAVLW--VLVIGS--LVARWLLGIQGGFCFR 164  
Db 123 LVSIDRYALVKTMSGMGRVRAKLYSLVINGCTLLSSPMLVFRMTKYSDEG----- 178  
Qy 165 STRHN-----FNSMRFPFLGFLYFLAVVFCSLKVVTTALAQRPPTDVGQA 209  
Db 179 --HNVTAQVTSYPSLTIWVFTNMLNVVGLPLSVITFTCTQIMQVLRNNEKQKFEI 235  
Qy 210 EATKAKRMVWNLVVFVVCFLPLHVLTV-----RLAVGNACALLETTIRRALYITSKLS 265  
Db 236 QTERATVTLVWVLLFLICWLPQISTFDTLRLGLI--LSSCQDERIIDVITQIASPMA 294

Qy 266 DANCCLDAICYYNWAKSFQEAR 287  
Db 295 YSNSCLNPLVYVIVGKFRFKS 316

## RESULT 12

## OORTB2

bradykinin receptor type B-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: A41283; A55079; S47529

R:McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Oberholte, R.; Bach, C.; Zuppan, P.; Fujita

Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991

A:Title: Expression cloning of a rat B-2 bradykinin receptor.

A:Reference number: A41283; MUID:91352062; PMID:1715575

A:Accession: A41283

A:Molecule type: mRNA

A:Residues: 1-366 <MCE>

A:Cross-references: UNIPROT:P25023; GB:M59967

R:Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.

J. Biol. Chem. 269, 26920-26925, 1994

A:Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence

A:Reference number: A55079; MUID:95014558; PMID:7929432

A:Accession: A55079

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-75,'A',77-366 <PBS>

A:Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190

R:Wang, D.; Ma, J.; Chao, L.; Chao, J.

Biochim. Biophys. Acta 1219, 171-174, 1994

A:Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.

A:Reference number: S47529; MUID:94368850; PMID:8086459

A:Accession: S47529

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-366 <WAN>

A:Cross-references: EMBL:L26173; NID:g476749; PIDN:AAAG2492.1; PID:g685244

C:Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;

F:31-48/Domain: transmembrane #status predicted <TM1>

F:79-96/Domain: transmembrane #status predicted <TM2>

F:107-126/Domain: transmembrane #status predicted <TM3>

F:154-170/Domain: transmembrane #status predicted <TM4>

F:197-215/Domain: transmembrane #status predicted <TM5>

F:245-261/Domain: transmembrane #status predicted <TM6>

F:314,182/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:105-186/Disulfide bonds: #status predicted

F:326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.3%; Score 311.5; DB 1; Length 366;  
Best Local Similarity 28.1%; Pred. No. 2.9e-21;  
Matches 90; Conservative 54; Mismatches 127; Indels 49; Gaps 9;

Qy 2 NGTYNTCGSSDLTWPPPAIKLGFYAYLGVLLVGLLNSLALVVFCCRMQOWTETRIYMTN 61  
Db 14 NGTSEVNCPTDEWWSMLNAIQAPFLWVFLAALENIFLVSVFCLHKTCTVAEYILGN 73

Qy 62 LAVADLCCLCTLPVLSLRDTS-----TPLCQLSQGIYLTNRYSISLVTIAVDRTVA 117  
Db 74 LAGADLILACGLPFWAITIANNFDWLFGEVLCRVVNTMIYNNLYSSICFLMLVSDRYLA 133

Qy 118 VRHPLRARGLRSPROAAVCAVLW--VLVIGS--LVARWLLGIQGGFCFRSTRN---- 169  
Db 134 LVKTMGMGRVRAKLYSLVINGCTLLSSPMLVFRMTKYSDEG-----HNVTAQ 186

Qy 170 -----FNSMRFPFLGFLYFLAVVFCSLKVVTTALAQRPPTDVGQAEATKAKRM 218  
Db 187 VIVYPSRSEWFTNMLNLVGLPLSLIITFTCTQIMQVLRNNEKQKFEVQTEKATVL 246

Qy 219 VWANLLVVFVVCFLPLHVLTV-----RLAVGNACALLETTIRRALYITSKLSD----A 267  
Db 236 QTERATVTLVWVLLFLICWLPQISTFDTLRLGLI--LSSCQDERIIDVITQIASPMA 294

Db 247 VLAVGLFVLCWFPPQISTFLTDLRLGLVSGCWN-----BRAVDIVTQISSVAYS 298

Qy 268 NCCDLAICYYYMAKEFOEAS 287

Db 299 NSCLNPLVYIVGKRRFKKS 318

RESULT 13

S13638

platelet-activating factor receptor - guinea pig

C:Species: Cavia porcellus (guinea pig)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S13638

R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To

Nature 349, 342-346, 1991

A:Title: Cloning by functional expression of platelet-activating factor receptor from gu

A:Reference number: S13638; MUID:91101726; PMID:1846231

A:Accession: S13638

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-342 <HON>

A:Cross-references: UNIPROT:P21556; GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443

A>Note: the species of guinea pig is not identified; in GenBank entry CCPAPREC, release

C:Superfamily: ATP receptor p2u

Query Match 19.1%; Score 309; DB 2; Length 342;

Best Local Similarity 28.2%; Pred. No. 4.7e-21;

Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

Qy 29 VLLVLGLLNSLALWVFCRMM---QQWTETRIYMTNLAVADLCCLCTLP--FVLHSLRDT 83

Db 24 IIFVGIITANGVWVF-ARLYPSKKNLEIKIPWNLTVADLLFTLPLWIVVYNSQGN 82

Qy 84 SDTP--LCQLSQGIYLTNRYMSISLVTAIAVDVYVVRHPLRAGRLSPQAAACAVLW 141

Db 83 WFLPKFLNAGCLFFINTYCSVAPLGVITNRFQAVKYPKTAQATTKRGIALSLIV 142

Qy 142 VLVIGSLVARWLIGQE-----GGFCFSTRHNNSMRPPL-----LGFYLP 185

Db 143 VAIWAA--ASFVLVNDSTNVVNSNKGAGNITRCFEHYEKGSKPVLIIHICIVLGFVFL 200

Qy 186 VVVFCSLKVVTALAQRPTDVGQAEATRAKRWVWVANLLVFVCPFLPHVGLTVRLAVGW 245

Db 201 LILFCNLVLIHTLLRQPVKQORNAEVRRLWVCTVLAVFVCFVPHM-----VQLPW 255

Qy 246 NACAL-----LETIRALYITSKLSANDACCLDAICYYYWAKEFOE 285

Db 256 TLAELGMWPNSSHOAINDAHOVTCLLSTNCVLDPVYICFLTCKKPK 302

RESULT 14

B57641

G protein-coupled receptor 4 - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004

C:Accession: B57641

R:Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.

Genomics 30, 84-88, 1995

A:Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome

A:Reference number: A57641; MUID:96129306; PMID:8595909

A:Accession: B57641

A>Status: preliminary; nucleic acid sequence not shown; translation not shown; significa

A:Molecule type: DNA

A:Residues: 1-362 <MAH>

A:Cross-references: UNIPROT:P50132; GB:U22108; NID:g722282; PIDN:AAA98458.1; PID:g722283

C:Genetics:

A:introns: #status absent

C:Superfamily: G protein-coupled receptor 4

C:Keywords: G protein-coupled receptor

Query Match 19.1%; Score 308.5; DB 2; Length 362;

Best Local Similarity 30.6%; Pred. No. 5.5e-21;

Matches 93; Conservative 48; Mismatches 114; Indels 49; Gaps 11;

Qy 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLLVGLLNSLALWVFCRMMQOWTETRIY 58

Db 3 NGTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLRLWAAVYRQORNELGVY 55

Qy 59 MTNLAVADLCCLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR 114

Db 56 LNLNSIADLLYICTLPLWVDYFLHHDNWIHGPQSGCKLFGFIFYTNIYISIAFLCCISVDR 115

Qy 115 YVAVRHPLRAGRLSPQAAACAVLWLVLTGS-----LVARWLLGIQEGGFCFRST-RHN 169

Db 116 YLAVAHPLRFAFLRRVKTAVAVSSVWVWATELGANSVLFHDEL-----FDRYNYHT 166

Qy 170 FNSMRPPL-----LGFYLPVAVVFCSLKVVTALAQRPTDVGQAEATRAKAK 216

Db 167 FCFEKFMEGWVAMNLYRVFVGFPLWMLLSYRGILRAVRGVSVT---EROEKAKIK 223

Qy 217 RMVWANLLVFVCPFLPHVGLTVRLAV-----GWNACALLETIRRALYITSKLSANDCCLD 272

Db 224 RLALSIAIVLCFAPYHVLLSRSVAVLGHMPWD-CGFEERVFSAYHSSLAFTSLNCVAD 282

Qy 273 AICY 276

Db 283 PILY 286

RESULT 15

S68207

G protein-coupled receptor 6C.1 - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S68207

R:An, S.; Tsai, C.; Goetzl, E.J.

FEBS Lett. 375, 121-124, 1995

A:Title: Cloning, sequencing and tissue distribution of two related G protein-coupled r

A:Reference number: S68207; MUID:96087098; PMID:7498459

A:Accession: S68207

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-362 <ANS>

A:Cross-references: UNIPROT:P46093; EMBL:U35399; NID:g1015420; PIDN:AAA79061.1; PID:g101

C:Superfamily: G protein-coupled receptor 4

C:Keywords: G protein-coupled receptor

Query Match 19.0%; Score 307.5; DB 2; Length 362;

Best Local Similarity 31.0%; Pred. No. 6.8e-21;

Matches 93; Conservative 49; Mismatches 117; Indels 41; Gaps 11;

Qy 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLLVGLLNSLALWVFCRMMQOWTETRIY 58

Db 3 NHTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLALWAAVYRQORNELGVY 55

Qy 59 MTNLAVADLCCLCTLP----FVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDR 114

Db 56 LNLNSIADLLYICTLPLWVDYFLHHDNWIHGPQSGCKLFGFIFYTNIYISIAFLCCISVDR 115

Qy 115 YVAVRHPLRAGRLSPQAAACAVLWLVLTGSISLVARWLLGIQEGGFCFRST-RHNFNSM 173

Db 116 YLAVAHPLRFAFLRRVKTAVAVSSVWVWATELGANSAP--LFHDE---LFRDRYNYHTFCFE 170

Qy 174 RFPL-----LGFYLPVAVVFCSLKVVTALAQRPTDVGQAEATRAKAKRWV 220

Db 171 KFPMEGWVAMNLYRVFVGFPLWMLLSYRGILRAVRGVSVT---EROEKAKIKRLAL 227

Qy 221 ANLAVFVVCFLPHVGLTVRLAV-----GWNACALLETIRRALYITSKLSANDCCLDACY 276

Db 228 SLIAIVLCFAPYHVLLSRSIAIVLGRPWD-CGFEERVFSAYHSSLAFTSLNCVADPILY 286

Search completed: May 23, 2005, 11:30:21

Job time : 18 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 11:07:54 ; Search time 63 Seconds  
(without alignments)  
1896.968 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGYNTCGSSDLTWPPAIK.....AVAPRAKHSQDSLCTVLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1615	100.0	309	5	ABG95172 Human GPC
2	1609	99.6	309	3	AAY79576 Human G p
3	1609	99.6	309	5	ABG95159 Human GPC
4	1609	99.6	309	6	ABP82002 Human G p
5	1609	99.6	309	7	ADB67656 Human G p
6	1609	99.6	309	8	ADO29394 Human GPC
7	1609	99.6	309	8	ADO78094 Human GPC
8	1603	99.3	309	3	AAY69989 Human rec
9	1603	99.3	547	7	ADf70461 Orphan re
10	1601	99.1	309	7	ADf50511 Human GPC
11	1597	98.9	309	3	AAY58645 Human G-p
12	1597	98.9	309	6	ADA84069 Human GPR
13	1597	98.9	394	8	ADO78095 Human GPR
14	1597	98.9	394	8	ADR10454 Human pro
15	1377	85.3	286	8	ADp29765 Human sec
16	1123	69.5	307	8	ADO29395 Mouse GPC
17	401	24.8	370	2	AAW62597 Human 7-t
18	401	24.8	370	5	ABP61511 Human NF-
19	401	24.8	370	6	ABG73513 Human p2y
20	401	24.8	370	6	ABP81870 Human G p
21	401	24.8	370	7	ADH69286 Human pur
22	401	24.8	370	8	ADf91778 Human p2y
23	401	24.8	370	8	ADO29049 Human nov
24	401	24.8	370	8	ADq88244 Human 241
25	401	24.8	370	8	ADQ81575 Human lys

26	401	24.8	608	7	ADf70491 Orphan re
27	400	24.8	370	7	ADH69285 Human pur
28	400	24.8	370	8	ADf91777 Human p2y
29	396	24.5	370	8	ADO29050 Mouse nov
30	391	24.2	370	5	ABP61510 Human NF-
31	388	24.0	327	8	ADO29415 Mouse GPC
32	377.5	23.4	363	5	AAU77993 Human inf
33	377.5	23.4	363	5	ADJ63782 Human G p
34	377.5	23.4	363	7	ADf28998 Human G p
35	376.5	23.3	362	6	ABG72358 Human orp
36	376.5	23.3	363	2	AAW94654 G-protein
37	376.5	23.3	363	4	AAU04379 Human G-p
38	376.5	23.3	363	7	ADc86215 Human GPC
39	376.5	23.3	363	7	ADL96482 Human G p
40	376.5	23.3	363	7	ADN38908 Cancer/an
41	376.5	23.3	363	8	ADM46118 Human 5-o
42	376.5	23.3	363	8	ADM46120 Human 5-o
43	376.5	23.3	363	8	ADN41887 Amino aci
44	376.5	23.3	363	8	ADO05575 Human hru
45	376.5	23.3	363	8	ADP04973 Human HM7

## ALIGNMENTS

## RESULT 1

ABG95172  
ID ABG95172 standard; protein; 309 AA.

XX AC ABG95172;

XX DT 04-DEC-2002 (first entry)

XX DE Human GPCR GPR35 mutant A216K.

XX KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychocatic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; receptor; mutant; muten.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200268600-A2.

XX PD 06-SEP-2002.

XX PF 26-FEB-2002; 2002WO-US005625.

XX PR 26-FEB-2001; 2001US-0271913P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JW;  
Lin I, Ortuno D;

XX DR WPI; 2002-706980/76.  
N-PSDB; ABS73401.

XX PT New human G-protein coupled receptor (GPCR), useful for screening agonist  
or inverse agonist compounds for treating diseases associated with GPCR.

XX PS Example 2; Page 189-190; 201pp; English.

XX CC The present invention relates to transmembrane receptors, particularly  
endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
endogenous) versions of the GPCRs, and the polynucleotide sequences  
encoding them. The GPCRs are useful for screening agonist or inverse  
agonist compounds for treating diseases associated with GPCR. Diseases  
that can be treated with such compounds include allergies, hypercension,  
reflux disease, depression, migraine, schizophrenia, ulcers, psychotic

CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents a mutant human GPCR

XX SQ Sequence 309 AA;

Query Match 100.0%; Score 1615; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-168;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPPAIKLGFAIYGLVLLVGLLLSLALWVFCRQQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPPPAIKLGFAIYGLVLLVGLLLSLALWVFCRQQTETRIYMT 60

QY 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120

QY 121 PLRARGLRSPQAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180  
 DB 121 PLRARGLRSPQAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240  
 DB 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKFOEASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTILA 309  
 DB 301 QDSLVCVTILA 309

## RESULT 2

AY79576  
 ID AAY79576 standard; protein; 309 AA.

XX AC AAY79576;

XX 15-AUG-2000 (first entry)

XX Human G protein coupled receptor GPR35.

XX GPR35; G protein coupled receptor; human; NIDDM1;  
 KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
 KW diagnosis; therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 174

FT /note= "encoded by GCG"

FT Misc-difference 234

FT /note= "encoded by AGT"

XX WO200023603-A2.

XX PN

XX PD

XX 27-APR-2000.

XX PF 21-OCT-1999; 99WO-US024890.

XX PR 21-OCT-1998; 98US-0105052P.

XX PR 13-MAY-1999; 99US-0134175P.

XX PA (ARCH-) ARCH DEV CORP.

XX PA (TEXA ) UNIV OF TEXAS SYSTEM.

XX PI Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;

XX PI Hanis CL, Bell GI, Cox NJ;

XX

DR WPI; 2000-339702/29.  
 DR N-PSDB; AAA27485, AAY79574, AAY79576.

XX Method for screening for type 2 diabetes mellitus comprises detecting a  
 PT polymorphism in a calpain encoding nucleic acid segment or a protease-  
 PT encoding nucleic acid segment.

XX Claim 75; Page 237-238; 257pp; English.

XX The present sequence is that of the human gene encoding G protein coupled  
 CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The  
 CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
 CC (34.1% identity) suggesting that ATP or other nucleotide is its ligand.  
 CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
 CC relatively higher levels in adult lung, small intestine, colon and  
 CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
 CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
 CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
 CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10  
 CC gene, which encodes a novel calpain-like cysteine protease, designated  
 CC calpain 10. Mutations in the CAPN10 gene are responsible for a  
 CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
 CC propensity for type 2 diabetes mellitus are based on detection of a  
 CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
 CC for identifying modulators of calpain activity, and using these  
 CC modulators to treat diabetes, in particular through the regulation of an  
 CC insulin secretory response or insulin mediated glucose transport

XX SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 3; Length 309;

Best Local Similarity 99.7%; Pred. No. 1e-167;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPPAIKLGFAIYGLVLLVGLLLSLALWVFCRQQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPPPAIKLGFAIYGLVLLVGLLLSLALWVFCRQQTETRIYMT 60

QY 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120

QY 121 PLRARGLRSPQAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180  
 DB 121 PLRARGLRSPQAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240  
 DB 181 YLPLAVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKFOEASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTILA 309

DB 301 QDSLVCVTILA 309

## RESULT 3

ABG95159

ID ABG95159 standard; protein; 309 AA.

XX AC ABG95159;

XX DT 04-DEC-2002 (first entry)

XX Human GPCR GPR35.

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
 KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
 KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
 KW myocardial infarction; MI; stroke; glaucoma; anxiety;

KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 KW prostatic hypertrophy; receptor.  
 XX Homo sapiens.  
 OS WO200268600-A2.  
 PN 06-SEP-2002.  
 XX 26-FEB-2002; 2002WO-US005625.  
 XX 26-FEB-2001; 2001US-0271913P.  
 XX (AREN-) ARENA PHARM INC.  
 PA Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX WPI; 2002-706980/76.  
 DR N-PSDB; ABS73345.  
 XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
 PT or inverse agonist compounds for treating diseases associated with GPCR.  
 XX Claim 29; Page 128-130; 201pp; English.  
 PS The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
 CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents an endogenous human GPCR  
 XX  
 SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 5; Length 309;  
 Best Local Similarity 99.7%; Pred. No. 1e-167;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 NMGTYNTCGSSDLTWPPAIKLGFAVYGLVGLVLLGLLLNSLALWVFCRQQMTETRIYMT 60  
 Db 1 NMGTYNTCGSSDLTWPPAIKLGFAVYGLVGLVLLGLLLNSLALWVFCRQQMTETRIYMT 60  
 Qy 61 NLAVADLCCLCTLPVLSLHSLRDTSDTLCQLSQGIYLTNRNMSISLVTIAVDRYVVRH 120  
 Db 61 NLAVADLCCLCTLPVLSLHSLRDTSDTLCQLSQGIYLTNRNMSISLVTIAVDRYVVRH 120  
 Qy 121 PLRAGLSPQAAVCAVAVLVITGSLVARWLLGIQGGFCFRSTRNENSMRPLLG 180  
 Db 121 PLRAGLSPQAAVCAVAVLVITGSLVARWLLGIQGGFCFRSTRNENSMRPLLG 180  
 Qy 181 YLPLAVVVFCSIKVVTALAQRPPTDVGQAEATRKAKRWANLLVVFVCFPLPHVGLTVR 240  
 Db 181 YLPLAVVVFCSIKVVTALAQRPPTDVGQAEATRKAKRWANLLVVFVCFPLPHVGLTVR 240  
 Qy 241 LAVGNACALLETIRRALYITSKLSNDANCCLDIAICYYYMAKEFQASALAVAPRAKAHS 300  
 Db 241 LAVGNACALLETIRRALYITSKLSNDANCCLDIAICYYYMAKEFQASALAVAPRAKAHS 300  
 Qy 301 QDSLVCVTLA 309  
 Db 301 QDSLVCVTLA 309

## RESULT 4

ABP82002

ID ABP82002 standard; protein; 309 AA.

XX

AC ABP82002;  
 XX 04-MAR-2003 (first entry)  
 DT Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.  
 DE G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 XX G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX Homo sapiens.  
 OS WO200261087-A2.  
 XX 08-AUG-2002.  
 XX 19-DEC-2001; 2001WO-US050107.  
 XX 19-DEC-2000; 2000US-0257144P.  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 PA Burner GC, Roush CL, Brown JP;  
 PI WPI; 2003-046718/04.  
 DR N-PSDB; ABZ42852.  
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX Sequence 309 AA;

## Query Match

Best Local Similarity 99.6%; Score 1609; DB 6; Length 309;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 QY 121 PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLG 180  
 DB 121 PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLG 180  
 QY 181 YLPLAVVVFCSLKVVYTAQAORPTDVGQAETRAKRMVWNLVYVVCFLPLHVGLTVR 240  
 DB 181 YLPLAVVVFCSLKVVYTAQAORPTDVGQAETRAKRMVWNLVYVVCFLPLHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFQASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFQASALAVAPRAKHS 300  
 QY 301 QDSLVCVTLA 309  
 DB 301 QDSLVCVTLA 309

## RESULT 5

ADB67656  
 ID ADB67656 standard; protein; 309 AA.

AC ADB67656;

DT 04-DEC-2003 (first entry)

DE Human G protein-coupled receptor 35, SEQ ID 25.

KW Cardiant; Gene therapy; heart failure; human;

KW G protein-coupled receptor 35; receptor.

XX Homo sapiens.

XX WO2003072824-A1.

XX PD 04-SEP-2003.

XX PF 27-FEB-2003; 2003WO-JP002228.

XX PR 28-FEB-2002; 2002JP-00054388.

XX PR 15-APR-2002; 2002JP-00112228.

XX PA (SANY ) SANKYO CO LTD.

XX PI Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

XX PI Koishi R, Nakamatsu K;

XX DR WPI; 2003-679959/64.

XX DR N-PSDB; ADB67672.

XX PT Predicting pathological conditions in heart failure using marker genes  
 and proteins.

XX PS Claim 1; Page 111-113; 137pp; Japanese.

XX CC The present invention relates to a method for predicting pathological  
 conditions in heart failure using expression of one of 17 gene sequences  
 (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-  
 ADB67662). The proteins and genes are useful for diagnosis, treatment and  
 prevention of heart failure.

XX SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 1e-167;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 DB 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 QY 121 PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLG 180  
 DB 121 PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLG 180  
 QY 181 YLPLAVVVFCSLKVVYTAQAORPTDVGQAETRAKRMVWNLVYVVCFLPLHVGLTVR 240  
 DB 181 YLPLAVVVFCSLKVVYTAQAORPTDVGQAETRAKRMVWNLVYVVCFLPLHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFQASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFQASALAVAPRAKHS 300  
 QY 301 QDSLVCVTLA 309  
 DB 301 QDSLVCVTLA 309

## RESULT 6

ADO29394  
 ID ADO29394 standard; protein; 309 AA.

XX ADO29394;

XX DT 29-JUL-2004 (first entry)

XX DE Human GPCR GPR35, SEQ ID NO:496.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 transgenic mouse; neurological disorder; adrenal gland disorder;  
 colon disorder; intestinal disorder; cardiovascular disorder;  
 muscular disorder; blood disorder; immune disorder; bone disorder;  
 joint disorder; metabolic disorder; nutritive disorder; cancer;  
 kidney disorder; liver disorder; lung disorder; breast disorder;  
 ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 cytostatic; antiinflammatory; vasotropic; antiangiogenic; antiarrhythmic;  
 CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
 dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 receptor.

XX OS Homo sapiens.

XX PN WO2004040000-A2.

XX PD 13-MAY-2004.

XX PF 09-SEP-2003; 2003WO-US028226.

XX PR 09-SEP-2002; 2002US-0409303P.

XX PR 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX PA Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX PI Madisen L, Meilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WIPI; 2004-390329/36.

XX DR N-PSDB; ADO29916.

XX PT Novel mammalian G protein coupled receptors, useful for identifying



PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
PS Claim 151; SEQ ID NO 496; 542pp; English.  
XX  
XX The invention relates to human and mouse G protein-coupled receptors  
XX (GPCRs) and nucleic acids encoding them. The invention also relates to  
XX sequences at least 90% identical to the GPCR proteins and nucleic acids  
XX of the invention; methods of treating, preventing or diagnosing diseases  
XX associated with GPCRs of the invention; methods of screening for  
XX compounds useful in the treatment of GPCR-related diseases; a transgenic  
XX mouse comprising a GPCR gene of the invention; a mouse comprising a  
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
XX from the transgenic mice; kits comprising several mice, each of which has  
XX a mutation in a different GPCR gene of the invention; and kits comprising  
XX probes which hybridize to GPCR polynucleotides of the invention. The  
XX invention further discloses variants of the GPCR polypeptides and vectors  
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
XX be used in the diagnosis, treatment or prevention of a wide variety of  
XX diseases including neurological disorders (e.g., Alzheimer's disease,  
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
XX disorders of the adrenal gland; disorders of the colon or intestine  
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
XX myocardial infarction); muscular disorders; blood disorders (e.g.,  
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,  
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the  
XX invention. Note: The full sequence data for this patent did not form part  
XX of the printed specification; those sequences not shown were obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 8; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
QY 61 NLAVADLCLLCTLPVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTIAVDRYVAVRH 120  
DB 61 NLAVADLCLLCTLPVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTIAVDRYVAVRH 120  
QY 121 PLRAGLSRPRQAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
DB 121 PLRAGLSRPRQAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
QY 181 YLPLAVVVFCSLKVVYLTALAQRPPTDVGQAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVYLTALAQRPPTDVGQAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300  
DB 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300  
QY 301 QDLSLCVTILA 309  
DB 301 QDLSLCVTILA 309

RESULT 7

ADO78094

ID ADO78094 standard; protein; 309 AA.

XX

AC ADO78094;  
XX 26-AUG-2004 (first entry)  
XX Human GPR35.  
XX  
XX tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
XX prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
XX ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
XX melanoma; tumour; human; GPR35.  
XX  
XX Homo sapiens.  
XX DE10254601-A1.  
XX 03-JUN-2004.  
XX 22-NOV-2002; 2002DE-01054601.  
XX 22-NOV-2002; 2002DE-01054601.  
XX (GANY-) GANYMED PHARM AG.  
XX Tuereci O, Sahin U, Koslowski M;  
XX WPI; 2004-421820/40.  
XX N-PSDB; ADO78086.  
XX  
XX Composition containing inhibitor of expression or activity of specific  
XX tumour-associated antigens, useful for treating cancers, also related  
XX compositions for diagnosis and monitoring.  
XX  
XX Claim 72; SEQ ID NO 9; 124pp; German.  
XX  
XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
XX or cervix, also melanoma. Compositions containing TAG, or related nucleic  
XX acid, antibodies or host cells, are also useful for diagnosis and  
XX monitoring of tumours. The present sequence represents the amino acid  
XX sequence of a human GPR35.  
XX  
XX Sequence 309 AA;  
Query Match 99.6%; Score 1609; DB 8; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
QY 61 NLAVADLCLLCTLPVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTIAVDRYVAVRH 120  
DB 61 NLAVADLCLLCTLPVLSLSDTSDTPLCQLSQGIYLTNRNYSISLVTIAVDRYVAVRH 120  
QY 121 PLRAGLSRPRQAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
DB 121 PLRAGLSRPRQAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
QY 181 YLPLAVVVFCSLKVVYLTALAQRPPTDVGQAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVYLTALAQRPPTDVGQAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300  
DB 241 LAVGNACALLETIRRALYITTSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHS 300  
QY 301 QDLSLCVTILA 309  
DB 301 QDLSLCVTILA 309

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Db      301 QDSLCTLA 309
RESULT 8
ID      AAY69989 standard; protein; 309 AA.
XX      AAY69989;
XX      AAY69989;
DT      31-MAY-2000 (first entry)
XX      Human receptor-associated protein from Incyte clone 3083742.
XX      Human receptor-associated protein; HRAP; Incyte clone 3083742;
KW      cytosolic; immunomodulatory; anti-inflammatory; cardiatic; antianaemic;
KW      antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW      antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW      neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW      cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW      gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW      arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW      multiple sclerosis; irritable bowel syndrome.
XX      Homo sapiens.
XX      Key
FH      Location/Qualifiers
FT      Modified-site 2 /note= "Potential N-glycosylation site"
FT      Modified-site 79 /note= "Potential phosphorylation site"
FT      Modified-site 98 /note= "Potential phosphorylation site"
FT      Modified-site 102..118 /note= "Potential phosphorylation site"
FT      Region /label= Signature sequence
FT      /note= "G-protein coupled receptor"
FT      Modified-site 129 /note= "Potential phosphorylation site"
FT      Modified-site 165 /note= "Potential phosphorylation site"
FT      Modified-site 191 /note= "Potential phosphorylation site"
FT      Modified-site 212 /note= "Potential phosphorylation site"
FT      Modified-site 238 /note= "Potential phosphorylation site"
FT      Modified-site 253 /note= "Potential phosphorylation site"
FT      Modified-site 261 /note= "Potential phosphorylation site"
FT      Modified-site /note= "Potential phosphorylation site"
XX      WO200008155-A2.
XX      17-FEB-2000.
XX      06-AUG-1999; 99WO-US017777.
XX      07-AUG-1998; 98US-0160065P.
XX      01-SEP-1998; 98US-0098703P.
XX      (INCY-) INCYTE PHARM INC.
XX      Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
XX      Corley NC, Baughn MR;
XX      WPI; 2000-205710/18.
XX      N-PSDB; AA250891.
XX      New human receptor-associated proteins (HRAP) useful for the diagnosis,
XX      treatment and prevention of cell proliferative, autoimmune, inflammatory,
XX      reproductive, cardiovascular, and gastrointestinal disorders.
XX      Claim 1; Page 76; 99pp; English.
XX
CC      The present sequence is human receptor-associated protein (HRAP) from
CC      Incyte clone 3083742 obtained from OVARUN01 cDNA library. This sequence
CC      is expressed in haematopoietic/immune, gastrointestinal and reproductive
CC      tissues. HRAP has cytosolic, immunomodulatory, antiinflammatory,
CC      cardiatic, antiarteriosclerotic, hepatotropic, antiarthritic,
CC      antirheumatic, osteopathic, antiallergic, antianaemic, antiasthmatic,
CC      neuroprotective, dermatological and neuroprotective activities. The present
CC      sequence is useful in the diagnosis, treatment and prevention of
CC      disorders associated with HRAP expression, especially cell proliferative,
CC      autoimmune/inflammatory, reproductive, cardiovascular and
CC      gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia,
CC      cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis,
CC      diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
XX
SQ      Sequence 309 AA;
Query Match 99.3%; Score 1603; DB 3; Length 309;
Best Local Similarity 99.4%; Pred. No. 4.7e-167;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 MNGTYNTCGSSDLTPPPAIIKLGFAVYGLVGLVGLLNSLALWVFCRMOQWTEIRIYMT 60
DB      1 MNGTYNTCGSSDLTPPPAIIKLGFAVYGLVGLVGLLNSLALWVFCRMOQWTEIRIYMT 60
QY      61 NLAVADLCLLCTLPFVLSLSDTSLPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120
DB      61 NLAVADLCLLCTLPFVLSLSDTSLPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120
QY      121 PLRARGLSRQAAAVCAVWLVLVIGSLVARWLLGIQEGGFCFSTRHNFNSMRPFLG 180
DB      121 PLRARGLSRQAAAVCAVWLVLVIGSLVARWLLGIQEGGFCFSTRHNFNSMRPFLG 180
QY      181 YLPLAVVVFCSLKVVYVLTALAQRPPTDVGQAEATRKAKRMVWVNLVYVVCFLPHVGLTVR 240
DB      181 YLPLAVVVFCSLKVVYVLTALAQRPPTDVGQAEATRKAKRMVWVNLVYVVCFLPHVGLTVR 240
QY      241 LAVGNACALLETIRRALYITSKLSDANCCLDALCYVYMAKEFOEASALAVAPRAKHS 300
DB      241 LAVGNACALLETIRRALYITSKLSDANCCLDALCYVYMAKEFOEASALAVAPRAKHS 300
QY      301 QDSLCTLA 309
DB      301 QDSLCTLA 309
RESULT 9
ADF70461
ID      ADF70461 standard; protein; 547 AA.
XX      AC ADF70461;
XX      DT 12-FEB-2004 (first entry)
XX      DE Orphan receptor ligand-related human protein SeqID84.
XX      KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
XX      KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
XX      KW GFPuv; Enhanced GFP; EGFP; human.
XX      OS Homo sapiens.
XX      PN WO2003071272-A1.
XX      PD 28-AUG-2003.
XX      PF 21-FEB-2003; 2003WO-JP001901.
XX      PR 22-FEB-2002; 2002JP-00045728.
XX      PR 23-JUL-2002; 2002JP-00213949.
XX      PR 11-OCT-2002; 2002JP-00298237.
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX

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PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
XX WPI; 2003-697654/66.  
DR N-PSDB; ADF70563.  
XX

PT Transformation of cells with a fusion protein of an orphan receptor  
PT protein with a fluorescent protein useful for identification of ligands  
PT to the orphan receptor.

XX  
XX  
PS Disclosure; SEQ ID NO 84; 594bp; Japanese.

XX This invention relates to a novel method of identifying ligands to an  
XX orphan receptor protein which comprises transforming cells with DNA  
XX encoding a fusion protein of the orphan receptor with a fluorescent  
XX protein, so that the fusion protein is expressed in the cells (or cell  
XX membranes isolated from them) and contacting the cells with the potential  
XX ligand to be tested. A suitable fluorescent protein for incorporation in  
XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
XX identification of ligands binding to an orphan receptor protein.

XX Sequence 547 AA;

Query Match 99.3%; Score 1603; DB 7; Length 547;

Best Local Similarity 99.4%; Pred. No. 9.6e-167;

Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNGYNTCGSSDLTPPPAIFGAYLGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

Db 1 MNGYNTCGSSDLTPPPAIFGAYLGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

Qy 61 NLAVADLCLLCTLPVLSLSDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Db 61 NLAVADLCLLCTLPVLSLSDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Qy 121 PLRAGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180

Db 121 PLRAGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180

Qy 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVFVVCFLPHVGLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVFVVCFLPHVGLTVR 240

Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOASALAVAPRAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOASALAVAPRAKHS 300

Qy 301 QDSLCTVTLA 309

Db 301 QDSLCTVTLA 309

RESULT 10

ADF50511

ID ADF50511 standard; protein; 309 AA.

XX

AC ADF50511;

DT 12-FEB-2004 (first entry)

XX Human GPCR GPR35 D113A mutein (SeqID 191).

XX mutant; mutein; transformation; endocrine cell line;

XX expression cloning system; bioactive peptide; GPCR ligand; human.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 113

FT /note= "Wild type Asp substituted by Ala"

XX WO2003087366-A1.

XX 23-OCT-2003.

XX 16-APR-2003; 2003WO-JP004840.

XX 16-APR-2002; 2002JP-00113030.

XX (KYOWA) KYOWA HAKKO KOGYO KK.

XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;  
XX Nishi T, Obinata M;

XX WPI; 2003-833737/77.

XX Endocrine cell lines originated from mammalian hypothalamus and  
XX pancreatic islet, applicable in expression cloning systems of bioactive  
XX peptide precursor genes, and in screening G protein-coupled receptor  
XX ligands.

XX Example 24; SEQ ID NO 191; 316pp; Japanese.

XX This invention relates to a novel method for obtaining a DNA that encodes  
XX a peptide acting as agonist, antagonist or inverse agonist on a target  
XX receptor. Specifically, it comprises transformation of endocrine cell  
XX lines originating from mammalian hypothalamus and pancreatic islets,  
XX culturing the transformants and contacting with cells expressing the  
XX target receptor. The identification of those cells with a response  
XX reaction can be used for selecting a transformant cell line with the  
XX appropriate target activity that is expressing the novel transformed DNA.  
XX Accordingly, the present invention describes novel cell lines that are  
XX applicable in expression cloning systems of bioactive peptide precursor  
XX genes, and in screening GPCR ligands for use as drugs including agonists,  
XX antagonists and inverse agonists i.e. activators and inhibitors. Such  
XX cell lines can provide a highly sensitive and convenient GPCR ligand  
XX assay system. This polypeptide sequence is the human GPCR GPR35 D113A  
XX mutein of the invention.

XX Sequence 309 AA;

Query Match 99.1%; Score 1601; DB 7; Length 309;

Best Local Similarity 99.4%; Pred. No. 7.8e-167;

Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNGYNTCGSSDLTPPPAIFGAYLGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

Db 1 MNGYNTCGSSDLTPPPAIFGAYLGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60

Qy 61 NLAVADLCLLCTLPVLSLSDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Db 61 NLAVADLCLLCTLPVLSLSDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Qy 121 PLRAGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180

Db 121 PLRAGLSRPRQAAAVCAVLVWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180

Qy 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVFVVCFLPHVGLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVFVVCFLPHVGLTVR 240

Qy 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOASALAVAPRAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOASALAVAPRAKHS 300

Qy 301 QDSLCTVTLA 309

Db 301 QDSLCTVTLA 309

RESULT 11

AAV58645

ID AAV58645 standard; protein; 309 AA.

XX

AC AAV58645;

XX 11-APR-2000 (first entry)

XX Human G-protein coupled receptor GPR35A.

XX GPR35A; human; G-protein coupled receptor; purinergic;  
 KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;  
 KW cytostatic; antidiabetic; anorectic; antitachymatic; antiparkinsonian;  
 KW hypotensive; hypertensive; osteopathic; antianginal; cardiant;  
 KW cerebroprotective; antiulcer; antiallergic; antimigraine; antienetic;  
 KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;  
 KW therapy; diagnosis; vaccine.

XX Homo sapiens.

XX ADA84069

XX WO9964452-A1.

XX 16-DEC-1999.

XX 01-JUN-1999; 99WO-US012123.

XX 11-JUN-1998; 98US-00096031.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Elshourbagy NA;

XX WPI; 2000-116525/10.

XX N-PSDB; AA235390.

XX New human GPR35A polypeptides and polynucleotides used to identify  
 PT agonists, antagonists and inhibitors for use in therapy.

XX Claim 1; Page 32-33; 38pp; English.

XX The present sequence represents human GPR35A, a novel member of the  
 CC purinergic family of polypeptides and a G-protein coupled receptor. The  
 CC invention provides GPR35A polypeptides having at least 70% identity with  
 CC the present sequence, GPR35A polynucleotides, recombinant materials, and  
 CC methods for their production. GPR35A polypeptides can be used for  
 CC identifying agonists and antagonists/inhibitors, and for detecting  
 CC diseases associated with inappropriate GPR35A activity or levels. GPR35A  
 CC polypeptides and polynucleotides, agonists, antagonists and antibodies  
 CC are used to treat: infections such as bacterial, fungal, protozoan and  
 CC viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;  
 CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart  
 CC failure; hypotension; hypertension; urinary retention; osteoporosis;  
 CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign  
 CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological  
 CC disorders including anxiety, schizophrenia, manic depression, depression,  
 CC delirium, dementia and severe mental retardation; and dyskinesias such as  
 CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also  
 CC useful for production of vaccines

XX Sequence 309 AA;

Query Match 98.9%; Score 1597; DB 3; Length 309;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-166;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCCSSDLTPPAIKGFAYGLVLLVGLLNSLAWVFCRCMOQNTETRIYMT 60  
 DB 1 MNGTYNTCCSSDLTPPAIKGFAYGLVLLVGLLNSLAWVFCRCMOQNTETRIYMT 60

QY 61 NLAVADCLLCTLPFVHLSLRDTSPTPLCQLSGQIYLTNRYMSISLVTAIVDRYVAVRH 120  
 DB 61 NLAVADCLLCTLPFVHLSLRDTSPTPLCQLSGQIYLTNRYMSISLVTAIVDRYVAVRH 120

QY 121 PLRARGLRSPRAAAVCAVLWLVIGSLVARMVLGTOEGGFCFRSTRHFNFSMRPFLG 180  
 DB 121 PLRARGLRSPRAAAVCAVLWLVIGSLVARMVLGTOEGGFCFRSTRHFNFSMRPFLG 180

QY 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFVVCFLPLHVGLTVR 240

Db 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFVVCFLPLHVGLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYTMAKEFOASALAVAPRAKAHS 300

Db 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYTMAKEFOASALAVAPRAKAHS 300

QY 301 QDSLCLVTILA 309

Db 301 QDSLCLVTILA 309

RESULT 12

ADA84069

ID ADA84069 standard; protein; 309 AA.

XX

AC ADA84069;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human GPR35 protein.

XX

KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;  
 KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;  
 KW vaccine.

XX

OS Homo sapiens.

XX

PN WO2002103028-A2.

XX

PD 27-DEC-2002.

XX

PF 30-MAY-2002; 2002WO-IB004189.

XX

PR 30-MAY-2001; 2001US-0293999P.

PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.

XX

PA (BIOM-) BIOMEDICAL CENT.

XX

PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;  
 N-PSDB; ADA84068.

DR

DR N-PSDB; ADA84068.

XX

PT Determining if a nucleic acid is a marker for a phenotype/cell type of  
 PT interest, by global comparison of expressed sequence tags known to be  
 PT expressed in the phenotype/cell type with all ESTs expressed in normal  
 PT tissue.

XX

PS Claim 29; Page 448-449; 516pp; English.

XX

CC The invention relates to a novel method for determining if a nucleic acid  
 CC is a marker for a predetermined phenotype/cell type of interest from a  
 CC biological species. The method comprises performing a global comparison  
 CC of a group of expressed sequence tags (ESTs) known to be expressed in the  
 CC phenotype/cell type of interest with all ESTs expressed in normal tissue  
 CC in order to identify ESTs that are preferentially expressed in the  
 CC phenotype/cell of interest. A method of the invention is useful for  
 CC determining whether a nucleic acid is a marker for a predetermined  
 CC phenotype or cell type of interest from a biological species, preferably  
 CC Arabidopsis or human. The cell type of interest is an abnormal cell such  
 CC as a tumour cell, and the predetermined phenotype is a stress-induced  
 CC phenotype such as hyperosmotic stress or high salt conditions. A method  
 CC of the invention is also useful for determining the progression of colon  
 CC cancer in a human, for detecting a tumour cell, and for regulating or  
 CC preventing the growth of a tumour cell. An antibody of the invention is  
 CC useful for detecting the absence or presence of peptides encoded by  
 CC tumour-associated markers. A polypeptide of the invention is useful as an  
 CC immunogen for vaccinating an animal. The present sequence represents a  
 CC tumour-associated antigen of the invention.

XX Sequence 309 AA;

Query Match 98.9%; Score 1597; DB 6; Length 309;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-166;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120  
 DB 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120

QY 121 PLRARGLSRPRQAAACAVLWLVITGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180  
 DB 121 PLRARGLSRPRQAAACAVLWLVITGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180

QY 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTILA 309  
 DB 301 QDSLVCVTILA 309

RESULT 13  
 ADO78095  
 ID ADO78095 standard; protein; 394 AA.  
 XX AC ADO78095;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Human GPR35 isoform.  
 XX KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
 KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
 KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
 KW melanoma; tumour; human; GPR35.  
 XX OS Homo sapiens.  
 XX PN DE10254601-A1.  
 XX PD 03-JUN-2004.  
 XX PF 22-NOV-2002; 2002DE-01054601.  
 XX PR 22-NOV-2002; 2002DE-01054601.  
 XX PA (GANY-) GANYMED PHARM AG.  
 XX PI Tuereci O, Sahin U, Koslowski M;  
 XX WPI; 2004-421820/40.  
 XX Composition containing inhibitor of expression or activity of specific  
 PT tumour-associated antigens, useful for treating cancers, also related  
 PT compositions for diagnosis and monitoring.  
 XX Claim 72; SEQ ID NO 10; 124pp; German.  
 XX The invention relates to pharmaceutical compositions that comprise an  
 CC agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of TAG, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney

CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the amino acid  
 CC sequence of a human GPR35.  
 XX SQ Sequence 394 AA;  
 Query Match 98.9%; Score 1597; DB 8; Length 394;  
 Best Local Similarity 99.0%; Pred. No. 2.9e-166;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 86 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWTETRIYMT 145  
 QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120  
 DB 146 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 205

QY 121 PLRARGLSRPRQAAACAVLWLVITGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 180  
 DB 206 PLRARGLSRPRQAAACAVLWLVITGSLVARWLLGIQEGGFCFRSTRNFNSMRPPLIGF 265

QY 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
 DB 266 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 325

QY 241 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300  
 DB 326 LAVGNACALLETIRRALYITSKLSANDCCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 385

QY 301 QDSLVCVTILA 309  
 DB 386 QDSLVCVTILA 394

RESULT 14  
 ADR10454  
 ID ADR10454 standard; protein; 394 AA.  
 XX AC ADR10454;  
 XX DT 04-NOV-2004 (first entry)  
 XX DE Human protein useful for treating neurological disease Seq 3960.  
 XX KW human; oligo-capping method; diagnostic marker; gene therapy;  
 KW osteoporosis; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; dementia; short memory; cancer;  
 KW sense or motor function; emotional reaction; fear response; panic;  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
 KW tranquiliser.  
 XX OS Homo sapiens.  
 XX PN EP1447413-A2.  
 XX PD 18-AUG-2004.  
 XX PF 12-FEB-2004; 2004EP-00003145.  
 XX PR 14-FEB-2003; 2003JP-00102207.  
 XX PR 09-MAY-2003; 2003JP-00131452.  
 XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
 XX WPI; 2004-583265/57.  
 XX DR N-PSDB; ADR10415.  
 XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX Claim 1; SEQ ID NO 3960; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteoprotective, neuroprotective, neurotropic, antiparkinsonian,  
CC cytotstatic and tranquiliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
CC office.

XX SQ Sequence 394 AA;

Query Match 98.9%; Score 1597; DB 8; Length 394;  
Best Local Similarity 99.0%; Pred. No. 2.9e-166;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVLGLLLSLALWVFCRMOQWTETRIYMT 60  
DB 86 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVLGLLLSLALWVFCRMOQWTETRIYMT 145  
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
DB 146 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 205  
QY 121 PLRARGLSRPROAAVCAVLVLTGSLVARWLLGTOEGGFCFRSTRHNFNSMRPFLG 180  
DB 206 PLRARGLSRPROAAVCAVLVLTGSLVARWLLGTOEGGFCFRSTRHNFNSMAFPFLG 265  
QY 181 YLPLAVVVFCSLKVVTAALQRPPTDVGQAEATRKARVMWNLVFCFLPLHVGLTVR 240  
DB 266 YLPLAVVVFCSLKVVTAALQRPPTDVGQAEATRKARVMWNLVFCFLPLHVGLTVR 325  
QY 241 LAVGNACALLETRIRALYITSKLSNDANCLDAICYVYMAKEFQESALAVAPRAKAHS 300  
DB 326 LAVGNACALLEMIRREALYITSKLSNDANCLDAICYVYMAKEFQESALAVAPRAKAHS 385  
QY 301 QBSLCVTLA 309  
DB 386 QBSLCVTLA 394

RESULT 15  
ADP29765  
ID ADP29765 standard; protein; 286 AA.

XX AC ADP29765;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human secreted protein SEQ ID #532.  
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
XX KW cancer; inflammatory; immune; human secreted protein.  
XX OS Homo sapiens.  
XX PN WO2004035732-A2.  
XX DT 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467206P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486466P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486896P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX PA

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS  
PS Claim 1; SEQ ID NO 1763; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
SQ Sequence 286 AA;  
  
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Best Local Similarity 99.2%; Pred. No. 2.8e-142;  
Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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Qy 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMWVANLLVFVVCFLPHVGLTVR 240  
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Qy 241 LAVGNACALLETIRRALYITSKLSD 266  
Db |||||||  
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Db |||||||

Search completed: May 23, 2005, 11:27:39  
Job time : 64 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:30:27 ; Search time 3734 Seconds  
(without alignments)  
9480.388 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	922	99.1	930	AY401607	AY401607 Homo sapi
C 2	736.4	79.2	876	CN834209	CN834209 AGENCOURT
C 3	674.2	72.5	906	CN835542	CN835542 AGENCOURT
C 4	609.8	65.6	960	CN843697	CN843697 AGENCOURT
C 5	601.2	64.6	750	C0921772	C0921772 AGENCOURT
C 6	591.2	63.6	642	AY401608	AY401608 Pan trogl
C 7	581.8	62.6	778	C0923163	C0923163 AGENCOURT
C 8	571	61.4	759	C0957219	C0957219 AGENCOURT
C 9	549.2	59.1	924	AY401609	AY401609 Mus muscu
C 10	549.2	59.1	2849	AK036503	AK036503 Mus muscu
C 11	544.4	58.5	3158	AK034870	AK034870 Mus muscu
C 12	538.2	57.9	4254	AK089198	AK089198 Mus muscu
C 13	531.2	57.1	783	CN835586	CN835586 AGENCOURT
C 14	516.6	55.5	717	C0923285	C0923285 AGENCOURT
C 15	512.6	55.1	1019	CN832122	CN832122 AGENCOURT
C 16	510.6	54.9	777	C0921660	C0921660 AGENCOURT
C 17	510.4	54.9	1009	BB609892	BB609892 AGENCOURT
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C 19	458	49.2	592	BM772486	BM772486 K-EST0056
C 20	415	44.6	827	CN843490	CN843490 AGENCOURT
C 21	392.6	42.2	614	BZ221309	BZ221309 CH230-312
C 22	374.4	40.3	690	BY747772	BY747772 BY747772
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C 26	317.6	34.2	444	2	AW854188	AW854188 RC3-CT025
C 27	317	34.1	429	2	AW854178	AW854178 RC3-CT025
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C 29	313.4	33.7	648	7	C0957232	C0957232 AGENCOURT
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C 34	300.8	32.3	448	2	AW854198	AW854198 RC3-CT025
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C 37	296	31.8	571	2	BE696051	BE696051 RC3-CT025
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C 39	293.4	31.5	701	6	CB321988	CB321988 UI-CF-FNO
C 40	293	31.5	585	2	AW854051	AW854051 RC3-CT025
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ALIGNMENTS

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LOCUS Homo sapiens GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY401607  
VERSION AY401607.1 GI:39757596  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 930)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 930)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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VERSION CN843697.1 GI:47949352
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 960)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB13 row: a column: 02
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Location/Qualifiers
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varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."

FEATURES
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Best Local Similarity 98.1%; Pred. No. 8.2e-123;
Matches 617; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 348 GGCCTGTGCGGCACCCCGCTCGTGTGCCCGCGGCTGCGGTCCCCAGCAGGCTGCGGCCGT 407
DB 573 GGCCTGTGCGGCACCCCGCTCGTGTGCCCGCGGATGCGGTCCCCAGCAGGCTGCGGCCGT 514

QY 408 GTGCGCGGTCTCTGCGGTGCTGTGTCATCGGCTCCCTGTGGTGGCTCGCTCGTGGGAT 467
DB 513 GTGCGCGGTCTCTGCGGTGCTGTGTCATCGGCTCCCTGTGGTGGCTCGCTCGTGGGAT 454

QY 468 TCAGGAGGGCGGTCTCTGCTTACGAGGACCCGGGCACAATTCACTCCATCGGTTCCC 527
DB 453 TCAGGAGGGCGGTCTCTGCTTACGAGGACCCGGGCACAATTCACTCCATCGGTTCCC 394

QY 528 GCTGTCTGGGATTTACTGTCCCTCGGCGGTGGTGTCTTCTGTCTCCCTGAAGTGGTGAC 587
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QY 588 TGCCCTTGCCGACGAGGCCACCCACGACGTGGGGCAGGAGGCCACCCGCGAGGCTTAA 647
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QY 708 GCTGACAGTGGCCTCGCAGTGGGTGGGAGCGCTGTGGCTCTCTGGAGACCATCGTGG 767
Db 213 GCTGACAGTGGCCTCGCAGTGGGTGGGAGCGCTGTGGCTCTCTGGAGACCATCGTGG 154
QY 768 CGCCCTGTACATAACCAAGCAAGTCTCAGATGCCAACTGTCTCTGGAGCCCATCTGCTA 827
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Db 33 GGGCCACAAAAGCCAGGACTCTCTGTGGG 5

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DEFINITION AGENCOURT_30698404 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7211833 3', mRNA sequence.
ACCESSION CO921772
VERSION CO921772.1 GI:51272514
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 750)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB15 row: d column: 11
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varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 64.6%; Score 601.2; DB 7; Length 750;
Best Local Similarity 97.0%; Pred. No. 6.1e-121;
Matches 612; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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VERSION	AY401608.1 GI:39757597		
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ORGANISM	Pan troglodytes		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
TITLE	1. (bases 1 to 642)		
JOURNAL	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		
PUBMED	Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,		
REFERENCE	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
AUTHORS	Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous		
JOURNAL	gene trios		
PUBMED	Science 302 (5652), 1960-1963 (2003)		
REFERENCE	14671302		
AUTHORS	2. (bases 1 to 642)		
TITLE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,		
JOURNAL	Todd,M.A., Tanenbaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,		
PUBMED	Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,		
REFERENCE	Adams,M.D. and Cargill,M.		
AUTHORS	Direct Submission		
TITLE			



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Qy 914 GGTGACCTCGCCTA 929
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genomic survey sequence.
ACCESSION AY401609
VERSION AY401609.1 GI:39757598
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 924)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 924)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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ORIGIN

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Matches 704; Conservative 0; Mismatches 193; Indels 9; Gaps 3;

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[illegible]



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ORIGIN

Query Match 57.9%; Score 538.2; DB 3; Length 4254;  
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DB 748 CATTGCTGTGACCGCTATGTGGCAGTGGCGCATCCCTGCTGCTGCTGCTGCTGCTGCT 807  
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QY 447 GGCTCGCTGGCTGGGGGATTCAGAGGGGGGCTTCTGCTTCAGAGGCTGCTGCTGCT 503  
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RESULT 13

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IMAGE:7001933 5', mRNA sequence.  
ACCESSION CN835586  
VERSION CN835586.1 GI:47941241  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 783)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
cDNA Library Arrayed by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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Location/Qualifiers  
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clone and include the following: 5'-EcoRV-XmaI/XhoI-3',  
5'-EcoRV-XmaI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat)  
a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 57.1%; Score 531.2; DB 7; Length 783;  
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QY 181 AACCTGGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
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CO923285.1 GI:51275562
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE 1. (bases 1 to 717)
JOURNAL NIH-MGC http://mgi.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."
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ORIGIN

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EST.
SOURCE Homo sapiens (human)
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CO9232122
AGENCOURT_15864152 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001931 3', mRNA sequence.
CO9232122
CO9232122.1 GI:47935875
EST.
SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 1019)  
AUTHORS NIH-MGC <http://mgc.mci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
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clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat)  
a Note: this is a NIH\_MGC Library."

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 930  
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Scoring table: IDENTITY\_NUC  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	925.2	99.5	930	15	Sequence 15, Appl
4	925.2	99.5	930	15	Sequence 491, App
5	920.4	99.0	1875	9	Sequence 6, Appl
6	920.4	99.0	1875	9	Sequence 21, Appl
7	920.4	99.0	1875	15	Sequence 350, App
8	916.8	98.6	24477	19	Sequence 1, Appli
9	900	96.8	1989	15	Sequence 17827, A
10	200.6	21.6	201	19	Sequence 636, App
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15	200.6	21.6	201	19	US-10-741-600-61567	Sequence 61567, A
16	200.6	21.6	201	19	US-10-741-600-61568	Sequence 61568, A
17	197.4	21.2	201	19	US-10-741-600-61525	Sequence 61525, A
18	197.4	21.2	201	19	US-10-741-600-61532	Sequence 61532, A
19	197.4	21.2	201	19	US-10-741-600-61535	Sequence 61535, A
20	195.8	21.1	201	19	US-10-741-600-61565	Sequence 61565, A
21	172.6	18.6	201	19	US-10-741-600-61546	Sequence 61546, A
22	150.6	16.2	201	19	US-10-741-600-61524	Sequence 61524, A
23	141.8	15.2	1854	10	US-09-866-050A-596	Sequence 596, App
24	141.8	15.2	1854	14	US-10-152-661-596	Sequence 596, App
25	111.6	12.0	1098	15	US-10-251-385-225	Sequence 225, App
26	111.2	12.0	1089	15	US-10-251-385-3	Sequence 3, Appli
27	111.2	12.0	1089	15	US-10-267-811-1	Sequence 1, Appli
28	111.2	12.0	1365	15	US-10-101-510-17	Sequence 17, Appl
29	111.2	12.0	1365	17	US-10-305-720-1429	Sequence 1429, Ap
30	111.2	12.0	1365	18	US-10-283-975A-113	Sequence 113, App
31	111.2	12.0	2693	10	US-09-850-948-1	Sequence 1, Appli
32	111.2	12.0	2693	15	US-10-273-575-1	Sequence 1, Appli
33	111.2	12.0	2696	15	US-10-225-567A-272	Sequence 272, App
34	111.2	12.0	2980	15	US-10-101-510-456	Sequence 456, App
35	110.4	11.9	1617	14	US-10-167-192-2	Sequence 2, Appli
36	110.4	11.9	1617	17	US-10-400-991-5	Sequence 5, Appli
37	110	11.8	1098	10	US-09-850-948-5	Sequence 5, Appli
38	110	11.8	1098	15	US-10-251-385-117	Sequence 117, App
39	110	11.8	1098	15	US-10-273-575-5	Sequence 5, Appli
40	110	11.8	1098	15	US-10-225-567A-282	Sequence 282, App
41	110	11.8	1434	16	US-10-029-386-25332	Sequence 25332, A
42	110	11.8	1697	14	US-10-109-533A-1	Sequence 1, Appli
43	110	11.8	1697	15	US-10-288-222A-11	Sequence 11, Appl
44	109.6	11.8	1089	15	US-10-251-385-165	Sequence 165, App
45	107.6	11.6	1254	18	US-10-484-788-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-10-083-168-84  
; Sequence 84, Application US/10083168  
; Publication No. US20030023069A1  
; GENERAL INFORMATION:  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Maciejewski-Lenior, Dominique  
; APPLICANT: Leonard, James N.  
; APPLICANT: Ortuno, Daniel  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Acr  
; FILE REFERENCE: AREN-0320  
; CURRENT APPLICATION NUMBER: US/10/093,168  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: No. US20030023069A1el Sequence  
US-10-083-168-84

Query Match 100.0%; Score 930; DB 14; Length 930;  
Best Local Similarity 100.0%; Pred. No. 2e+225;  
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCACTTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 60

DB 1 ATGATGGCACTTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCATCAAG 60





Qy	841	AAGGAGTCCAGGAGGCGCTCTGCACCTGGCGTCCCGTCTAGGCCCCACCAAGC	900
Db	841	AAGGAGTCCAGGAGGCGCTCTGCACCTGGCGTCCCGTCTAGGCCCCACCAAGC	900
Qy	901	CAGGACTCTCTGCGTGACCTCGCCATA	930
Db	901	CAGGACTCTCTGCGTGACCTCGCCATA	930

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RESULT 3
US-10-225-567A-491
; Sequence 491, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Cienna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-491

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Query Match	99.5%	Score 925.2;	DB.15;	Length 930;
Best Local Similarity	99.7%	Pred. No. 3.2e-224;		
Matches 927; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	1	ATGAATGGCACTTA	CAACAACCTGTGGCTCC	AGAGACCTCACCTGGCCCCCAGCGATCAAG	60
Db	1	ATGAATGGCACTTA	CAACAACCTGTGGCTCC	AGAGACCTCACCTGGCCCCCAGCGATCAAG	60
Qy	61	CTGGGCTTCTAGCC	TACTTGGGCGTCTGCT	TGGTGTAGGCCTGTGCTCAACAGCGCTG	120
Db	61	CTGGGCTTCTAGCC	TACTTGGGCGTCTGCT	TGGTGTAGGCCTGTGCTCAACAGCGCTG	120
Qy	121	GGCTCTGGGTCTT	CTGTGCTGCCGATG	CAGCAGTGGACGGAGACCCGCATCTACATGACC	180
Db	121	GGCTCTGGGTCTT	CTGTGCTGCCGATG	CAGCAGTGGAGACCCGCATCTACATGACC	180
Qy	181	AACCTGGCGGTGCC	GAACCTCTGCTGTG	CGACCTTGCCCTTCGTGCTGCTACCTCCCTG	240
Db	181	AACCTGGCGGTGCC	GAACCTCTGCTGTG	CGACCTTGCCCTTCGTGCTGCTACCTCCCTG	240
Qy	241	CGAGACACCTCAGA	CACGGCGGTGTCAG	GTCTCCAGAGGCATCTACCTGACCAACAGG	300
Db	241	CGAGACACCTCAGA	CACGGCGGTGTCAG	GTCTCCAGAGGCATCTACCTGACCAACAGG	300
Qy	301	TACATGAGCATCAG	CTGGTCAAGGCCAT	CGCCGTGGACCGCTATGTGGCCGTGGCGCAC	360
Db	301	TACATGAGCATCAG	CTGGTCAAGGCCAT	CGCCGTGGACCGCTATGTGGCCGTGGCGCAC	360
Qy	361	CGCTCGTCCCGGGG	CTGGGTTCCTCCAGG	CAGGCTGGCGCGGTGTCGCGGCTCTC	420
Db	361	CGCTCGTCCCGGGG	CTGGGTTCCTCCAGG	CAGGCTGGCGCGGTGTCGCGGCTCTC	420
Qy	421	TGGGTGCTGGTCA	TCCGGTCTCCGTG	GTCTGGCTCTCGGGGATTCAGGAGGGCGGC	480
Db	421	TGGGTGCTGGTCA	TCCGGTCTCCGTG	GTCTCGGGGATTCAGGAGGGCGGC	480
Qy	481	TTCTGCTTTCAGG	AGCACCGGGCACAAT	TTTCAACTCCATGGGTTCCCGTCTGGGATTC	540
Db	481	TTCTGCTTTCAGG	AGCACCGGGCACAAT	TTTCAACTCCATGGGTTCCCGTCTGGGATTC	540

541	Qy	TAC	TGCC	CCCT	GGCG	CGTG	GGTCTT	CTG	CCCTG	AAGGTGGT	GACTG	CCCTGG	CCCG	500
541	Db	TAC	TGCC	CCCT	GGCG	CGTG	GGTCTT	CTG	CCCTG	AAGGTGGT	GACTG	CCCTGG	CCCG	600
601	Qy	AGG	CCAC	CCCA	CGAC	GTGG	GGCAG	CGAG	GAGGCC	ACCCG	CAAGGCT	AAACG	CATGCT	660
601	Db	AGG	CCAC	CCCA	CGAC	GTGG	GGCAG	CGAG	GAGGCC	ACCCG	CAAGGCT	CCCG	CATGCT	660
661	Qy	GCC	AAC	CTC	CTG	GTG	TTC	TG	CCCTG	CA	CGTGGG	GCTG	AC	720
661	Db	GCC	AAC	CTC	CTG	GTG	TTC	TG	CCCTG	CA	CGTGGG	GCTG	AC	720
721	Qy	CTG	CGA	GTGGG	CTG	GAAG	CGCTG	CCCTC	CTG	GAGACG	ATCCG	TCGCG	CCCTG	780
721	Db	CTG	CGA	GTGGG	CTG	GAAG	CGCTG	CCCTC	CTG	GAGACG	ATCCG	TCGCG	CCCTG	780
781	Qy	ACC	AG	CAAG	CTC	T	CAG	ATG	CCAA	CTG	TG	CCCTG	GAGCG	840
781	Db	ACC	AG	CAAG	CTC	T	CAG	ATG	CCAA	CTG	TG	CCCTG	GAGCG	840
841	Qy	AAG	GAG	TTT	CC	AGG	AGG	CGT	CTG	CA	CTG	GC	CGTCC	900
841	Db	AAG	GAG	TTT	CC	AGG	AGG	CGT	CTG	CA	CTG	GC	CGTCC	900
901	Qy	CAG	GAC	TCT	CTG	TG	CGGTG	A	CCCT	CG	CCCTAA	930		
901	Db	CAG	GAC	TCT	CTG	TG	CGGTG	A	CCCT	CG	CCCTAA	930		

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RESULT 4
US-10-696-639-6
; Sequence 6, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bournier, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 930
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-6

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Query Match	99.5%	Score	925.2	DB 19	Length	930
Best Local Similarity	99.7%	Pred. No.	3.2e-224			
Matches	927	Conservative	0	Mismatches	3	Indels
						Gaps
						0
Qy	1	ATGAATGGCACCTTACAACACCTCTGGCTCCAGCGACCTACACCTGGCGCCCCCAGCGATCAAG	60			
Db	1	ATGAATGGCACCTTACAACACCTCTGGCTCCAGCGACCTACCTGGCGCCCCCAGCGATCAAG	60			
Qy	61	CTGGGCTTCTACGCCCTACTTTGGCGCTCTCTGGTCTAGGCCTGTGCTTCAACAGCCTG	120			
Db	61	CTGGGCTTCTACGCCCTACTTTGGCGCTCTCTGGTCTAGGCCTGTGCTTCAACAGCCTG	120			
Qy	121	CGCGCTCTGGGTGTTCTGCTCCGCGATGCAGCAGTGCAGGAGACCCGCATCTCATATGACC	180			
Db	121	CGCGCTCTGGGTGTTCTGCTCCGCGATGCAGCAGTGCAGGAGACCCGCATCTCATATGACC	180			
Qy	181	AACCTGCGGTGGCGACCTCTGCCTGCTGTGCACCTTGGCCCTTCTGTGCTGCACCTCCCTG	240			
Db	181	AACCTGCGGTGGCGACCTCTGCCTGCTGTGCACCTTGGCCCTTCTGTGCTGCACCTCCCTG	240			
Qy	241	CGAGACACCTTCAGACACGCCGCTGTGCAGCTCTCCCGAGGCATCTACCTGACCAACAGG	300			

241	CGAGACACCTCAGACACGCCGCTGTCAGACTCTCCAGAGGCATCTACCTGACCAACAGG	300
301	TACATGAGCATCAGCTGGTCAACGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC	360
301	TACATGAGCATCAGCTGGTCAACGCCATCGCCGTGGACCGCTATGTGGCCGTGCGGCAC	360
361	CGCGTGGTCCCGGGGTGGGTCCCCAGGACAGGCTGGCGCGTGTGGCGGCGTCTTC	420
361	CGCGTGGTCCCGGGGTGGGTCCCCAGGACAGGCTGGCGCGTGTGGCGGCGTCTTC	420
421	TGGGTCTGGTCACTCGGCTCCCTGGTGGCTCGCTGGGTCTCTGGGGATTCAGAGAGGGCGGC	480
421	TGGGTCTGGTCACTCGGCTCCCTGGTGGCTCGCTGGGTCTCTGGGGATTCAGAGAGGGCGGC	480
481	TTCTGTCTTCAGGAGCACCCGGGACAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC	540
481	TTCTGTCTTCAGGAGCACCCGGGACAATTTCAACTCCATGCGGTTCCCGCTGCTGGGATTC	540
541	TACCTGCCCTTGGCGTGTGTCTTCCTGCTCCCTGAAGTGTGTGACTGCCCTGGGCCACG	600
541	TACCTGCCCTTGGCGTGTGTCTTCCTGCTCCCTGAAGTGTGTGACTGCCCTGGGCCACG	600
601	AGGCCACCCACCGACGTGGGGCAGGCAGAGGCCACCCGCAAGGCTAAACGATGGTCTGG	660
601	AGGCCACCCACCGACGTGGGGCAGGCAGAGGCCACCCGCAAGGCTAAACGATGGTCTGG	660
661	GCCAACTCTCTGGTGTGTGGTGTCTTCTGCTGCCCTGACGCTGGGGCTGACAGTGGCC	720
661	GCCAACTCTCTGGTGTGTGGTGTCTTCTGCTGCCCTGACGCTGGGGCTGACAGTGGCC	720
721	CTCGCAGTGGGTGGAAACCCCTGTGCCCTCTCTGGAGACGATCCGCTCGCGCCCTGTACATA	780
721	CTCGCAGTGGGTGGAAACCCCTGTGCCCTCTCTGGAGACGATCCGCTCGCGCCCTGTACATA	780
781	ACAGCAAGCTCTCAGATGCCAACTGTCTGCTGTGACGCCATCTGCTACTACTACATGGCC	840
781	ACAGCAAGCTCTCAGATGCCAACTGTCTGCTGTGACGCCATCTGCTACTACTACATGGCC	840
841	AAGGAGTTTCAGAGGCGTCTGCATCTGGCGGTGGTCCCGTGTCTAAGGGCCCAACAAAGC	900
841	AAGGAGTTTCAGAGGCGTCTGCATCTGGCGGTGGTCCCGTGTCTAAGGGCCCAACAAAGC	900
901	CAGGACTCTCTGGGTGACCTTCGCCTTAA	930
901	CAGGACTCTCTGGGTGACCTTCGCCTTAA	930

## RESULT 5

US-09-768-877-21

; Sequence 21, Application US/09768877

; Patent No. US20020150896A1

**GENERAL INFORMATION:**

APPLICANT: POLONSKY, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

APPLICANT: ODA, NAOHISA

; APPLICANT: COX, NANCY J.

APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG

APPLICANT: BELL, GRAEME

FILE REFERENCE: ABCD-207

; FILE REFERENCE: ARCD:307  
: CURRENT APPLICATION NUMBER:

;  
 ;  
 ; CURRENT APPLICATION NUMBER: US/09/168,877  
 ; CURRENT FILING DATE: 2001-01-23

; CURRENT FILING DATE: 2001-01-23  
 : PRIOR APPLICATION NUMBER: 09/422

; PRIOR AFFILIATION NUMBER: 03/422,803  
 : PRIOR FILING DATE: 1999-10-21

; ERROR FILING DATE: 1993-10-21  
; NUMBER OF SEQ ID NOS: 30; NUMBER OF SEQ ID NOS: 30  
: SOFTWARE: PatentIn Ver. 2

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; COL INITS: FACCHEN VCL: Z.V
; SEQ ID NO 21

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; LENGTH: 1875

TYPE: DNA

ORGANISM:

US-09-768-877-21

Query Match 99.0%; Score 920.4; DB 9; Length 1875;

Best Local Similarity 99.4%; Pred. No. 5.3e-223;

Matches	924;	Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY	1	ATGAATGGCACCTACACACCTGTGGCTCAGCGACTCACCCTGGCCCCCAGCGATCAAG	60
DB	576	ATGAATGGCACCTACACACCTGTGGCTCAGCGACTCACCCTGGCCCCCAGCGATCAAG	635
QY	61	CTGGGCTTCTACGCTACTATTGGGCGTCTCTGGTGTAGGCTCTGTCTCAACAGCGCTG	120
DB	636	CTGGGCTTCTACGCTACTATTGGGCGTCTCTGGTGTAGGCTCTGTCTCAACAGCGCTG	695
QY	121	CGGCTCTGGGTGTCTGCTCCGATGACAGAGTGGACGGAGACCCGCACTCTATCATGACC	180
DB	696	CGGCTCTGGGTGTCTGCTCCGATGACAGAGTGGACGGAGACCCGCACTCTATCATGACC	755
QY	181	AACCTGGGGTGGCGACACTCTGCGTGTGTGCACTTGGCCCTTGTGTGTGCACTCCCTG	240
DB	756	AACCTGGGGTGGCGACACTCTGCGTGTGTGCACTTGGCCCTTGTGTGTGCACTCCCTG	815
QY	241	CGAGACACCTCAGACACGCGCTGTGCACTCTCCAGGCGCATCTACCTGACCAACAGG	300
DB	816	CGAGACACCTCAGACACGCGCTGTGCACTCTCCAGGCGCATCTACCTGACCAACAGG	875
QY	301	TACATGAGCATCAGCCTGTGTACGGCCATCGCCGTGGACCGCTATGTGGCCGTCCGAC	360
DB	876	TACATGAGCATCAGCCTGTGTACGGCCATCGCCGTGGACCGCTATGTGGCCGTCCGAC	935
QY	361	CCGCTGCTGCCCGCGGGCTCGGCTCCCCCAGCAGGCTGGGCGGTGTGGCGGTCCTC	420
DB	936	CCGCTGCTGCCCGCGGGCTCGGCTCCCCCAGCAGGCTGGGCGGTGTGGCGGTCCTC	995
QY	421	TGGGTGTGTGTATCGGCTCCCTGGTGGCTCGTGGCTCCTGGGGATTACAGGAGGGCGCG	480
DB	996	TGGGTGTGTGTATCGGCTCCCTGGTGGCTCGTGGCTCCTGGGGATTACAGGAGGGCGCG	1055
QY	481	TTCTGCTTCAGGAGCACCCCGGCACAAATTTCAACTCCATGCGGTTCCCGCTGTGGGATTC	540
DB	1056	TTCTGCTTCAGGAGCACCCCGGCACAAATTTCAACTCCATGCGGTTCCCGCTGTGGGATTC	1115
QY	541	TACCTGCGCCCTGGCGGTGGTCTTCTGCTCCCTGAAAGTGTGTGACTGCCCTGGGCCAG	600
DB	1116	TACCTGCGCCCTGGCGGTGGTCTTCTGCTCCCTGAAAGTGTGTGACTGCCCTGGGCCAG	1175
QY	601	AGGCCACCCACCGACGTGGGGCAGCAGAGGCACACCGCAAGGCTAAACGCATGCTGTGG	660
DB	1176	AGGCCACCCACCGACGTGGGGCAGCAGAGGCACACCGCAAGGCTGTCCCGCATGGTCTGG	1235
QY	661	GCCAACTCTCTGGTGTGTGTGTGTCTTCTGCCCCGTGACGTGGGGCTGACAGTGGCG	720
DB	1236	GCCAACTCTCTGGTGTGTGTGTGTCTTCTGCCCCGTGACGTGGGGCTGACAGTGGCG	1295
QY	721	CTCCGAGTGGGCTGAACCGCTGTGCCCTCTCTGGAGACGATCCGTGGCGCCCTGTACATA	780
DB	1296	CTCCGAGTGGGCTGAACCGCTGTGCCCTCTCTGGAGACGATCCGTGGCGCCCTGTACATA	1355
QY	781	ACCAGCAAGCTCTCAGATGCGCACTGTGCTGGACGCCATCTGTCTACTACTACATGGCC	840
DB	1356	ACCAGCAAGCTCTCAGATGCGCACTGTGCTGGACGCCATCTGTCTACTACTACATGGCC	1415
QY	841	AAGAGTTTCCAGGAGGCGTGTGCACTGGCCGTGGCTCCCCGTGTCTAAGGCCCAAAAAGC	900
DB	1416	AAGAGTTTCCAGGAGGCGTGTGCACTGGCCGTGGCTCCCCGTGTCTAAGGCCCAAAAAGC	1475
QY	901	CAGACCTCTGTGGGTGACCCCTCGCCCTAA	930
DB	1476	CAGACCTCTGTGGGTGACCCCTCGCCCTAA	1505

## RESULT 6

US-10-157-031-350

Sequence 350, Application US/10157031  
Publication No. US20030108890A1  
GENERAL INFORMATION:  
APPLICANT: Baranova, A. V.  
APPLICANT: Yankovsky, N. K.  
APPLICANT: Kozlov, A. P.  
APPLICANT: Lobashev, A. V.  
APPLICANT: Krukovskaya, L. L.  
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
FILE REFERENCE: 2760-103  
CURRENT APPLICATION NUMBER: US/10/157,031  
CURRENT FILING DATE: 2002-05-30  
NUMBER OF SEQ ID NOS: 415  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 350  
LENGTH: 1875  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-157-031-350

Query Match	99.0%;	Score 920.4;	DB 15;	Length 1875;
Best Local Similarity	99.4%;	Pred. No. 5.3e-223;		
Matches	924;	Conservative 0;	Mismatches 6;	Indels 0; Gaps 0;
Qy	1	ATGNAATGGCACCTACAACACTGTGGCTTCAGACGACCTCACCTGGCCCCCAGCGATCAAG	60	
Db	576	ATGAATGGCACCTACAACACTGTGGCTTCAGACGACCTCACCTGGCCCCCAGCGATCAAG	635	
Qy	61	CTGGGCTTCTACGCTACTTCTGGGCGTCTCTGTGTGTAGGCGCTGTGCTCAACAGCGCTG	120	
Db	636	CTGGGCTTCTACGCTACTTCTGGGCGTCTCTGTGTGTAGGCGCTGTGCTCAACAGCGCTG	695	
Qy	121	GCCTCTGGGTGTTCGTGTCGCCGATGCAGCAGTGGACGGAGACCCGCGATCTACATGACC	180	
Db	696	GCCTCTGGGTGTTCGTGTCGCCGATGCAGCAGTGGACGGAGACCCGCGATCTACATGACC	755	
Qy	181	AACCTGGCGTGGCCGACCTCTGCCTGTGTGCACCTTGCCTTCGTGTGCATCTCCCTG	240	
Db	756	AACCTGGCGTGGCCGACCTCTGCCTGTGTGTGCACCTTGCCTTCGTGTGCATCTCCCTG	815	
Qy	241	CGAGACACTCAGACAGCCGCGTGTGCAGCTCTCCAGGGCATCTACCTGACCAACAGG	300	
Db	816	CGAGACACTCAGACAGCCGCGTGTGCAGCTCTCCAGGGCATCTACCTGACCAACAGG	875	
Qy	301	TACATGAGCATACGCTGGTTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGGCGAC	360	
Db	876	TACATGAGCATACGCTGGTTCACGGCCATCGCCGTGGACCGCTATGTGGCCGTGGCGAC	935	
Qy	361	CCGCTGCGTGCCCGCGGGCTCGCGTCCCGACAGGAGGCTGGCGCGTGTGGCGGTCTCTC	420	
Db	936	CCGCTGCGTGCCCGCGGGCTCGCGTCCCGACAGGAGGCTGGCGCGTGTGGCGGTCTCTC	995	
Qy	421	TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCGCTGGGTCTCTGGGGAATTCAGAGGGCGC	480	
Db	996	TGGGTGCTGGTTCATCGGCTCCCTGGTGGCTCGCTGGGTCTCTGGGGAATTCAGAGGGCGC	1055	
Qy	481	TTCTGCTTCAGGAGCACCCGSCACAAATTCAACTCCATGCGGTTCCCGCTCTCGGATTC	540	
Db	1056	TTCTGCTTCAGGAGCACCCGSCACAAATTCAACTCCATGCGGTTCCCGCTCTCGGATTC	1115	
Qy	541	TACCTGCCCTTGGCGGTGGTCTTCTGCTCCCTGAAAGTGGTGAATGCGCCCTGGCCCGAG	600	
Db	1116	TACCTGCCCTTGGCGGTGGTCTTCTGCTCCCTGAAAGTGGTGAATGCGCCCTGGCCCGAG	1175	
Qy	601	AGGCCACCCACGACGTGGGCGAGGACAGGCCACCCGCAAGGCTTAACCGCATGCTCTGG	660	
Db	1176	AGGCCACCCACGACGTGGGCGAGGACAGGCCACCCGCAAGGCTTAACCGCATGCTCTGG	1235	
Qy	661	GCCAACTCTCTGGTGTTCGTGCTTCTGTCCTCTGACGTGGGGCTGCACAGTGGCG	720	
Db	1236	GCCAACTCTCTGGTGTTCGTGCTTCTGTCCTCTGACGTGGGGCTGCACAGTGGCG	1295	
Qy	721	CTCGACGTGGGCTGGAAACGCGCTGTGCCCTCTCTGGAGACGATCCCGTGGCGCCCTGTACATA	780	

RESULT 7  
US-09-768-877-1  
; Sequence 1, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/768,877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422,869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 49136  
; TYPE: DNA  
; ORGANISM: Human  
US-09-768-877-1

Query Match	99.0%;	Score 920.4;	DB 9;	Length 49136;
Best Local Similarity	99.4%;	Pred. No. 5.5e-223;		
Matches 924;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy 1	ATGAATGGACCTACAAACACCTGTGGCTCCAGAGACCTCACCTGGCCCCCAGCGATCAAG	60		
Db 43645	ATGAATGGACCTACAAACACCTGTGGCTCCAGAGACCTCACCTGGCCCCCAGCGATCAAG	43704		
Qy 61	CTGGGGCTTCTACGCTACTTTGGGCGTCTGCTGTGTGTAGGCGTGTGCTCAACAGCGCTG	120		
Db 43705	CTGGGGCTTCTACGCTACTTTGGGCGTCTGCTGTGTGTAGGCGTGTGCTCAACAGCGCTG	43764		
Qy 121	GGCTCTGGGTTTCTGCTGCCGATGACAGATGCGACGGAGACCGCATCTACATGACC	180		
Db 43765	GGCTCTGGGTTTCTGCTGCCGATGACAGATGCGACGGAGACCGCATCTACATGACC	43824		
Qy 181	AACCTGGCGTGGCGACACCTCTGCTGTGTGCACTTTCCTTCCTGCTGTCACCTCCCTG	240		
Db 43825	AACCTGGCGTGGCGACACCTCTGCTGTGTGCACTTTCCTTCCTGCTGTCACCTCCCTG	43884		
Qy 241	CGAGACACCTCAGACACGCCGTGTGCCAGCTCTCCACAGGCACTTACTTGACCAACAGG	300		
Db 43885	CGAGACACCTCAGACACGCCGTGTGCCAGCTCTCCACAGGCACTTACTTGACCAACAGG	43944		
Qy 301	TACATGAGCATCAGCTGTGTACGSCCATTCGCCGTGGACCGCTATGTGGCCGTGCGGCAC	360		
Db 43945	TACATGAGCATCAGCTGTGTACGSCCATTCGCCGTGGACCGCTATGTGGCCGTGCGGCAC	44004		
Qy 361	CCGCTCGTCCCGCGGGTGGCGTTCGCCCGAGCAGGCTGCGGGCGTGTGCGCGGTCTC	420		



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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1912)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1928)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-101-510-636

Query Match      96.8%; Score 900; DB 15; Length 1989;
Best Local Similarity 99.2%; Pred. No. 7.6e-218;
Matches 925; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ATGAATGGCACTTACCAACACTGTGGCTCCAGGACCTCACTGGCCCCAGCGATCAAG 60
Db 214 ATGAATGGCACTTACCAACACTGTGGCTCCAGGACCTCACTGGCCCCAGCGATCAAG 273

QY 61 CTGGGCTTCTAGCCTACTTGGGCGTCTGCTGGTGTAGGCTGTGCTCAACAGCTG 120
Db 274 CTGGGCTTCTAGCCTACTTGGGCGTCTGCTGGTGTAGGCTGTGCTCAACAGCTG 333

QY 121 GCGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGAGGACCGCATCTACATGACC 180
Db 334 GCGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGAGGACCGCATCTACATGACC 393

QY 181 AACCTGGGGTGGCGGACCTTGCCTGTGTGACCTTGGCTTGTGCTGCACTCCCTG 240
Db 394 AACCTGGGGTGGCGGACCTTGCCTGTGTGACCTTGGCTTGTGCTGCACTCCCTG 453

QY 241 CGAGACA-CCTCAGACAGCCCGCTGTGCCAGTCTTCCAGGCGATCTACCTGACCAACAG 299
Db 454 CGAGACAGCTCAGACAGCCCGCTGTGCCAGTCTTCCAGGCGATCTACCTGACCAACAG 513

QY 300 GTACATGAGCATCAGCTGTGTCAGGCGCATCCGCTGGACCGCTATGTGGCGTGGCA 359
Db 514 GTACATGAGCATCAGCTGTGTCAGGCGCATCCGCTGGACCGCTATGTGGCGTGGCA 573

QY 360 CCGCTGTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
Db 574 CCGCTGTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 633

QY 419 TCTGGGTGCTGCTATCGGCTCCCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
Db 634 TCTGGGTGCTGCTATCGGCTCCCTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 693

QY 479 GCTTCTGCTTACAGGAGCACCGGCAATTTCAACTCCATCGGTTCCGCTGCTGGAT 538
Db 694 GCTTCTGCTTACAGGAGCACCGGCAATTTCAACTCCATCGGTTCCGCTGCTGGAT 753

QY 539 TCTACTGCCCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTGGCTGGCC 598
Db 754 TCTACTGCCCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTGGCTGGCC 813

QY 599 AGAGGCCACCCACGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 658
Db 814 AGAGGCCACCCACGAGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 873

QY 659 GGGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 718
Db 874 GGGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 933

QY 719 GCTTCGCTGCTGGTGAACGCTGTGCCCTCTCGAGACGATCCGTCGCGCCCTGTACA 778
Db 934 GCTTCGCTGCTGGTGAACGCTGTGCCCTCTCGAGACGATCCGTCGCGCCCTGTACA 993

QY 779 TAACAGCAAGCTCTCAGATGCCAATCTGCTGCTGAGCGCCATCTGCTACTACTATGG 838
Db 994 TAACAGCAAGCTCTCAGATGCCAATCTGCTGCTGAGCGCCATCTGCTACTACTATGG 1053

QY 839 CCAAGAGTTCCAGGAGGCTGTGCACTGGCGCTGGCTCCCGCTGCTGAAGGCCACAAA 898
Db 939 CCAAGAGTTCCAGGAGGCTGTGCACTGGCGCTGGCTCCCGCTGCTGAAGGCCACAAA 941
```

```
Db 1054 CCAAGAGTTCCAGGAGGCTGTGCACTGGCGCTGGCTCCCGTGAAGGCCACAAA 1113

QY 899 GCCAGGACTCTCTGTGCGTGACCCCTGCGCTAA 930
Db 1114 GCCAGGACTCTCTGTGCGTGACCCCTGCGCTAA 1145

RESULT 10
US-10-741-600-61537
; Sequence 61537, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61537
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61537

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 223 TTCGTGCTGCACTCCCTGGGAGACACCTCAGACACGCGCTGTGCGAGCTCTCCAGGGC 282
Db 1 TTCGTGCTGCACTCCCTGGGAGACACCTCAGACACGCGCTGTGCGAGCTCTCCAGGGC 60

QY 283 ATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTCAGCCATCGCCGTGACCGC 342
Db 61 ATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTCAGCCATCGCCGTGACCGC 120

QY 343 TATGTGGCGGTGGGACACCCGCTGCTGCTGCGCGGCTGCGGTCCCGAGGAGGCTGCG 402
Db 121 TATGTGGCGGTGGGACACCCGCTGCTGCTGCGCGGCTGCGGTCCCGAGGAGGCTGCG 180

QY 403 GCGGTGTGGCGGTCTCTGG 423
Db 181 GCGGTGTGGCGGTCTCTGG 201

RESULT 11
US-10-741-600-61547
; Sequence 61547, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61547
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61547

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GTGGCTCCAGGACCTCACTGGCGCCCGAGCGATCAAGCTGGCTTCTACGCTACTTGG 82
Db 1 GTGGCTCCAGGACCTCACTGGCGCCCGAGCGATCAAGCTGGGCTTCTACGCTACTTGG 60
```

QY 83 GCGTCTGTGTCTAGCGCTGCTGCTCAACAGCCTGCGCTCTGGGTGTTCTGCTGCC 142  
|||||  
Db 61 GCGTCTGTGTCTAGCGCTGCTGCTCAACAGCCTGCGCTCTGGGTGTTCTGCTGCC 120  
|||||  
QY 143 GCATCAGCAGTGGAGCGGAGACCCGCTCTACATACCAACCTGGCGGTGGCCGACCTCT 202  
|||||  
Db 121 GCATCAGCAGTGGAGCGGAGACCCGCTCTACATACCAACCTGGCGGTGGCCGACCTCT 180  
|||||  
QY 203 GCTGCTGTGCACCTGGCCCT 223  
|||||  
Db 181 GCTGCTGTGCACCTGGCCCT 201  
|||||

RESULT 12  
US-10-741-600-61549  
; Sequence 61549, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61549  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-61549

Query Match 21.6%; Score 200.6; DB 19; Length 201;  
Best Local Similarity 99.5%; Pred. No. 4.7e-41;  
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 276 CCAGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGGCCATCGCGGT 335  
Db 1 CCAGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGGCCATCGCGGT 60  
|||||  
QY 336 GGACCGCTATGTGGCGTGGCGACCCCGCTGGGTGCGCGGGCTGCGGTCCCGCAGGCA 395  
Db 61 GGACCGCTATGTGGCGTGGCGACCCCGCTGGGTGCGCGGGCTGCGGTCCCGCAGGCA 120  
|||||  
QY 396 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTGCGGTGCTGCTGCGGTGCTGCTG 455  
Db 121 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTGCGGTGCTGCTGCGGTGCTGCTG 180  
|||||  
QY 456 GCTCCTGGGGATTTCAGGAGG 476  
Db 181 GCTCCTGGGGATTTCAGGAGG 201  
|||||

RESULT 13  
US-10-741-600-61551  
; Sequence 61551, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61551  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-61551

Query Match 21.6%; Score 200.6; DB 19; Length 201;  
Best Local Similarity 99.5%; Pred. No. 4.7e-41;  
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 558 TGGGCCCAACCTCTCTGGTGTCTGCTTCTCTGCTTCTGCCCCCTGCAGTGGGGCTGACATG 717  
Db 1 TGGGCCCAACCTCTCTGGTGTCTGCTTCTCTGCTTCTGCCCCCTGCAGTGGGGCTGACATG 60  
|||||  
QY 718 GCGCTCGCAGTGGGCTGGAACGCTGTGCCCTCTCTGGAGAGCATCCGTGCGGCCCTGTAC 777  
Db 61 GCGCTCGCAGTGGGCTGGAACGCTGTGCCCTCTCTGGAGAGCATCCGTGCGGCCCTGTAC 120  
|||||  
QY 778 ATAAACCAAGCAAGCTCTCAGATGCCAAGCTGCTTGGACGCCATCTGCTACTACTACATG 837  
Db 121 ATAAACCAAGCAAGCTCTCAGATGCCAAGCTGCTTGGACGCCATCTGCTACTACTACATG 180  
|||||  
QY 838 GCCAAGGAGTTCAGGAGGCG 858  
Db 181 GCCAAGGAGTTCAGGAGGCG 201  
|||||

RESULT 14  
US-10-741-600-61552  
; Sequence 61552, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 61552  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-61552

Query Match 21.6%; Score 200.6; DB 19; Length 201;  
Best Local Similarity 99.5%; Pred. No. 4.7e-41;  
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 273 CTCGCCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGGCCATCGC 332  
Db 1 CTCGCCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGGCCATCGC 60  
|||||  
QY 333 CQTGACCGCTATGTGGCGGTGCGGCACCCCGCTGGGTGCGCGGGCTGCGGTGCCCGCAG 392  
Db 61 CQTGACCGCTATGTGGCGGTGCGGCACCCCGCTGGGTGCGCGGGCTGCGGTGCCCGCAG 120  
|||||  
QY 393 GCAGCTCGGCGGTGCGCGGTCTCTGGGTGCTGCTGCGGTGCTGCTGCGGTGCTGCTGCTG 452  
Db 121 GCAGCTCGGCGGTGCGCGGTCTCTGGGTGCTGCTGCGGTGCTGCTGCGGTGCTGCTGCTG 180  
|||||  
QY 453 CTGGCTCCTGGGATTTCAGGA 473  
Db 181 CTGGCTCCTGGGATTTCAGGA 201  
|||||

RESULT 15  
US-10-741-600-61567  
; Sequence 61567, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61567
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61567

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GCCTGGCGCTCTGGGTGTTCTGCTGCGCATGCGACGTGGACGGAGACCGCATCTACA 175
Db 1 GCCTGGCGCTCTGGGTGTTCTGCTGCGCATGCGACGTGGACGGAGACCGCATCTACA 60

Qy 176 TGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGCAACCTTGCCCTTCGTGCTGCACT 235
Db 61 TGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGCAACCTTGCCCTTCGTGCTGCACT 120

Qy 236 CCCTGGCGAGACCTTCAGACACGGCGTGTGCGCAGCTCTCCAGGGCATCTACCTGACCA 295
Db 121 CCCTGGCGAGACCTTCAGACACGGCGTGTGCGCAGCTCTCCAGGGCATCTACCTGACCA 180

Qy 296 ACAGTACATGAGCATCAGCC 316
Db 181 ACAGTACATGAGCATCAGCC 201

Search completed: May 23, 2005, 14:50:03
Job time : 2851 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: May 23, 2005, 11:27:51 ; Search time 624 Seconds  
(without alignments)  
8822.691 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
Sequence: 1 atgaatgcacctaacaac.....tgtgcgtgacctgcctaa 930

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : N\_Geneseq\_16Dec04.\*
- 1: Geneseqn1980s.\*
  - 2: Geneseqn1990s.\*
  - 3: Geneseqn2000s.\*
  - 4: Geneseqn2001as.\*
  - 5: Geneseqn2001bs.\*
  - 6: Geneseqn2002as.\*
  - 7: Geneseqn2002bs.\*
  - 8: Geneseqn2003as.\*
  - 9: Geneseqn2003bs.\*
  - 10: Geneseqn2003cs.\*
  - 11: Geneseqn2003ds.\*
  - 12: Geneseqn2004as.\*
  - 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	930	6	ABST73401 DNA encod
2	925.2	99.5	930	6	ABST73345
3	925.2	99.5	930	8	ABZ42852 Human G p
4	925.2	99.5	930	9	ADb67672 Human G p
5	925.2	99.5	930	12	ADO29916 Human GPC
6	922	99.1	1369	3	AAZ50891 Human rec
7	920.4	99.0	1875	3	AAA27485 Human G p
8	920.4	99.0	1875	8	ADA84068 Human GPR
9	920.4	99.0	1875	12	ADO78086 Human GPR
10	920.4	99.0	49136	3	AAA27475 NIDDM1 re
11	919	98.8	1644	10	ADP70563 Orphan re
12	917.2	98.6	3811	13	ADR10415 Full leng
13	915.6	98.5	1043	3	AAZ35390 Human G p
14	900	96.8	1989	6	ABZ35525 Human gen
15	838	90.1	858	12	ADP28534 Human sec
16	549.2	59.1	924	12	ADO30206 Mouse GPC
17	141.8	15.2	1854	4	ADL10133 Mouse G p
18	141.8	15.2	1854	6	ABL35067 Murine cd
19	120.6	13.0	121	10	ADF87215 Single nu
20	111.6	12.0	1098	3	AAA30740 DNA encod

21	111.6	12.0	1098	10	ADC22744	Adc22744 Human G p
22	111.6	12.0	1098	10	ADH14217	Adh14217 Mutated h
23	111.2	12.0	1089	3	AAA30581	Aaa30581 Human G p
24	111.2	12.0	1089	6	AAD26832	Aad26832 Human G-p
25	111.2	12.0	1089	8	ACC78113	Acc78113 Human G p
26	111.2	12.0	1089	10	ADC22522	Adc22522 Human G p
27	111.2	12.0	1089	10	ADH13995	Adh13995 Human GPR
28	111.2	12.0	1089	12	ADO29766	Ado29766 Human nov
29	111.2	12.0	1365	6	ABZ34905	Abz34905 Human gen
30	111.2	12.0	1365	10	ADE84894	Ad84894 Farnesyl
31	111.2	12.0	1365	10	ACA56831	Ac56831 Human sig
32	111.2	12.0	1365	12	ADI56627	Adi56627 Human pol
33	111.2	12.0	2693	8	AAZ50858	Aaz50858 Human G-p
34	111.2	12.0	2696	8	ABZ42741	Abz42741 Human G p
35	111.2	12.0	2696	12	ADFI7570	Adfi7570 Human G p
36	111.2	12.0	2696	12	ADO28684	Ado28684 Human GPR
37	111.2	12.0	2932	6	AAD26831	Aad26831 Human G-p
38	111.2	12.0	2932	12	ADL71938	Adl71938 Human GPR
39	111.2	12.0	2932	13	ADS19844	Adsl19844 Human GPR
40	111.2	12.0	2980	6	ABZ35345	Abz35345 Human gen
41	110.8	11.9	2932	6	AAD26878	Aad26878 Human G-p
42	110.6	11.9	121	10	ADF87214	Adf87214 Single nu
43	110.4	11.9	970	2	AAZ10250	Aaz10250 cDNA enco
44	110.4	11.9	1149	5	AAS88030	Aas88030 DNA enco
45	110.4	11.9	1617	3	AAZ95037	Aaz95037 Human G p

ALIGNMENTS

RESULT 1  
ABS73401  
ID ABS73401 standard; DNA; 930 BP.  
AC ABS73401;  
XX  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE DNA encoding human GPCR GPR35 mutant A216K.

KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; Glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; mutant; ds.  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
XX WO200268600-A2.  
XX  
XX  
XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
XX Lin I, Ortuno D;

XX WPI; 2002-706980/76.

XX P-PSDB; ABG95172.

XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
XX or inverse agonist compounds for treating diseases associated with GPCR.

XX Example 2; Page 188-189; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly  
XX endogenous human G-protein coupled receptors (GPCRs), mutant (non-

CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
CC encoding them. The GPCRs are useful for screening agonist or inverse  
CC agonist compounds for treating diseases associated with GPCR. Diseases  
CC that can be treated with such compounds include allergies, hypertension,  
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence encodes a mutant human GPCR

XX SQ Sequence 930 BP; 141 A; 326 C; 278 G; 185 T; 0 U; 0 Other;

Query Match 100.0%; Score 930; DB 6; Length 930;

Best Local Similarity 100.0%; Pred. No. 1.9e-176;

Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGGCACTTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
DB |||||  
QY 1 ATGAATGGCACTTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
DB |||||  
QY 61 CTGGGCTTCTACGCTTACTTGGGCTCTGCTGTGGTGTAGGCTCTGCTCAACAGCCTG 120  
DB |||||  
QY 61 CTGGGCTTCTACGCTTACTTGGGCTCTGCTGTGGTGTAGGCTCTGCTCAACAGCCTG 120  
DB |||||  
QY 121 GCGCTCTGGGTCTTCTGCTGCCGATGACAGAGTGGACGAGACCGCATCTACATGACC 180  
DB |||||  
QY 121 GCGCTCTGGGTCTTCTGCTGCCGATGACAGAGTGGACGAGACCGCATCTACATGACC 180  
DB |||||  
QY 181 AACCTGGGGTGGCGACCTTGCCTGTGTGTGTCACCTTGGCCCTTGTGTGCACTCCCTG 240  
DB |||||  
QY 181 AACCTGGGGTGGCGACCTTGCCTGTGTGTGTCACCTTGGCCCTTGTGTGCACTCCCTG 240  
DB |||||  
QY 241 CGAGACACTCAGACACGCGCTGTGCCAGCTCTCCAGGCGATCTACTGTACCAACAGG 300  
DB |||||  
QY 241 CGAGACACTCAGACACGCGCTGTGCCAGCTCTCCAGGCGATCTACTGTACCAACAGG 300  
DB |||||  
QY 301 TACATGAGCATCAGCTGTGTGTCACGCTATGCGCGTGTGTCGCTGTGGCGAC 360  
DB |||||  
QY 301 TACATGAGCATCAGCTGTGTGTCACGCTATGCGCGTGTGTCGCTGTGGCGAC 360  
DB |||||  
QY 361 CGCGTGTGTCGCGGGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 420  
DB |||||  
QY 421 TGGGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480  
DB |||||  
QY 421 TGGGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480  
DB |||||  
QY 481 TTCTGTCTCAGGACACCGGACAAATTTCAATCTCATGCGGTTCCTGCTGTGGATTC 540  
DB |||||  
QY 481 TTCTGTCTCAGGACACCGGACAAATTTCAATCTCATGCGGTTCCTGCTGTGGATTC 540  
DB |||||  
QY 541 TACCTGCCCTTGGCGTGTGTCTTCTGCTCCCTGAAGTGTGACTGCCCTGGCCCCAG 600  
DB |||||  
QY 541 TACCTGCCCTTGGCGTGTGTCTTCTGCTCCCTGAAGTGTGACTGCCCTGGCCCCAG 600  
DB |||||  
QY 601 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB |||||  
QY 601 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
DB |||||  
QY 661 GCCAACCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB |||||  
QY 661 GCCAACCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
DB |||||  
QY 721 CTGCGAGTGGGTGGAACGCTGTGCCCTCTTGGAGAGCATCGGTGCGGCCCTGTACATA 780  
DB |||||  
QY 721 CTGCGAGTGGGTGGAACGCTGTGCCCTCTTGGAGAGCATCGGTGCGGCCCTGTACATA 780  
DB |||||  
QY 781 ACCAGCACTCTCAGATGCGCAACTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 840  
DB |||||  
QY 781 ACCAGCACTCTCAGATGCGCAACTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 840  
DB |||||  
QY 841 AAGGAGTTCCAGAGGCGCTGTGCACTGTGGCGTGGCTTCCCGTGTAAAGGCCCAAAAAGC 900

DB 841 AAGGAGTTCCAGAGGCGCTGTGCACTGTGGCGTGGCTTCCCGTGTAAAGGCCCAAAAAGC 900  
QY 901 CAGGACTCTCTGTGGTGACCTCGCCTAA 930  
DB 901 CAGGACTCTCTGTGGTGACCTCGCCTAA 930

## RESULT 2

ABS73345  
ID ABS73345 standard; cDNA; 930 BP.  
XX AC ABS73345;  
XX XX AC  
XX 04-DEC-2002 (first entry)  
XX XX  
XX cDNA encoding human GPCR GPR35.  
DE Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; gene; ss.  
XX Homo sapiens.  
XX OS  
XX WO200268600-A2.  
XX PD 06-SEP-2002.  
XX PF 26-FEB-2002; 2002WO-US005625.  
XX PR 26-FEB-2001; 2001US-0271913P.  
XX PA (AREN-) ARENA PHARM INC.  
XX PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
PI Lin I, Ortuno D;  
XX WPI; 2002-706980/76.  
DR P-PSDB; ABG95159.  
XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
PT or inverse agonist compounds for treating diseases associated with GPCR.  
XX Claim 31; Page 128; 201pp; English.  
XX The present invention relates to transmembrane receptors, particularly  
CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
CC encoding them. The GPCRs are useful for screening agonist or inverse  
CC agonist compounds for treating diseases associated with GPCR. Diseases  
CC that can be treated with such compounds include allergies, hypertension,  
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence encodes an endogenous human GPCR

SQ Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

Query Match 99.5%; Score 925.2; DB 6; Length 930;

Best Local Similarity 99.7%; Pred. No. 1.7e-175;

Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCACTTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
DB |||||  
QY 1 ATGAATGGCACTTACAACACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
DB |||||  
QY 61 CTGGGCTTCTACGCTTACTTGGGCTCTGCTGTGGTGTAGGCTCTGCTCAACAGCCTG 120  
DB 61 CTGGGCTTCTACGCTTACTTGGGCTCTGCTGTGGTGTAGGCTCTGCTCAACAGCCTG 120







Db 481 TTCTGCTTCAGAGACACCGGACAAATTTCAACTCCATCGGTTCCCGTCTGGGATTC 540  
Qy 541 TACCTGCCCTGGCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTCCCTGGCCGAG 600  
Db 541 TACCTGCCCTGGCGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTCCCTGGCCGAG 600  
Qy 601 AGGCCACCCACAGCTGGGGCAGCAGAGGCCACCGCAAGGCTAAAGCATGCTCTGG 660  
Db 601 AGGCCACCCACAGCTGGGGCAGCAGAGGCCACCGCAAGGCTGGCCGATGCTCTGG 660  
Qy 661 GCCAACCTCCTGGTGTCTGCTGCTTCTGCTCCCTGCACGTGGGGTGAACGTGGCC 720  
Db 661 GCCAACCTCCTGGTGTCTGCTGCTTCTGCTCCCTGCACGTGGGGTGAACGTGGCC 720  
Qy 721 CTCGAGTGGGTGGAAAGCCCTGTGCTCCCTCTGGAGAGATCCGTCGGCCCTGTACATA 780  
Db 721 CTCGAGTGGGTGGAAAGCCCTGTGCTCCCTCTGGAGAGATCCGTCGGCCCTGTACATA 780  
Qy 781 ACCAGAGCTCTCAGATGCCAAGCTGCTGCTGGAGAGATCCGTCGGCCCTGTACATGCC 840  
Db 781 ACCAGAGCTCTCAGATGCCAAGCTGCTGCTGGAGAGATCCGTCGGCCCTGTACATGCC 840  
Qy 841 AAGGAGTTCAGGAGCGTCTGCACCTGGCGGTGCTCCCGTCTAAAGGCCCAAAAGC 900  
Db 841 AAGGAGTTCAGGAGCGTCTGCACCTGGCGGTGCTCCCGTCTAAAGGCCCAAAAGC 900  
Qy 901 CAGGACTCTCTGCTGCTGACCTCGCCTAA 930  
Db 901 CAGGACTCTCTGCTGCTGACCTCGCCTAA 930

RESULT 6

AZ50891  
ID AZ50891 standard; cdna; 1369 BP.  
XX AC AZ50891;  
XX DT 31-MAY-2000 (first entry)  
XX DE Human receptor-associated protein cDNA from Incyte clone 3083742.  
XX KW Human receptor-associated protein; HRAP; Incyte clone 3083742;  
KW Cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic;  
KW antiatherosclerotic; hepatotropic; antiarthritic antirheumatic;  
KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;  
KW neuroprotective; diagnostic; treatment; prevention; reproductive disorder;  
KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;  
KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;  
KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;  
KW multiple sclerosis; irritable bowel syndrome; ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 45..974  
FT /\*tag= a  
FT /product= "HRAP"  
XX WO200008155-A2.  
XX PD 17-FEB-2000.  
XX PF 06-AUG-1999; 99WO-US017777.  
XX PR 07-AUG-1998; 98US-0160065P.  
XX PR 01-SEP-1998; 98US-0098703P.  
XX PA (INCY-) INCYTE PHARM INC.  
XX PI Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;  
PI Corley NC, Baughn MR;

DR WPI; 2000-205710/18.  
XX P-PSDB; AAY69989.  
PT New human receptor-associated proteins (HRAP) useful for the diagnosis,  
PT treatment and prevention of cell proliferative, autoimmune, inflammatory,  
PT reproductive, cardiovascular, and gastrointestinal disorders.  
XX Claim 9; Page 91; 99pp; English.  
XX The present sequence is a cDNA encoding human receptor-associated protein  
CC (HRAP) from Incyte clone 3083742 obtained from OVARTUN01 cDNA library.  
CC This sequence is expressed in haematopoietic/immune, gastrointestinal and  
CC reproductive tissues. HRAP has cytostatic, immunomodulatory,  
CC antiinflammatory, cardiant, antiatherosclerotic, hepatotropic,  
CC antiarthritic, antidiabetic, osteopathic, antiallergic, antianaemic,  
CC antiasthmatic, antidiabetic, dermatological and neuroprotective  
CC activities. The present sequence is useful in the diagnosis, treatment  
CC and prevention of disorders associated with HRAP expression, especially  
CC cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular  
CC and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis,  
CC leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma,  
CC dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable  
CC bowel syndrome)  
XX SQ Sequence 1369 BP; 245 A; 453 C; 424 G; 247 T; 0 U; 0 Other;  
Query Match 99.1%; Score 922; DB 3; Length 1369;  
Best Local Similarity 99.5%; Pred. No. 7.9e-175;  
Matches 925; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 ATGAATGGCACTCAACACACCTGTGGCTCCAGCGACCTCACCTGCGCCCGCCAGCATCAAG 60  
Db 45 ATGAATGGCACTCAACACACCTGTGGCTCCAGCGACCTCACCTGCGCCCGCCAGCATCAAG 104  
Qy 61 CTGGGCTTTACGCCCTACTTGGGGCTCTGCTGGTGTGCTAGGCTCTGCTCAACAGCCTG 120  
Db 105 CTGGGCTTTACGCCCTACTTGGGGCTCTGCTGGTGTGCTAGGCTCTGCTCAACAGCCTG 164  
Qy 121 GGGCTCTGGGTGTTCTGCTGCGCATGAGCAGATGAGAGCGGACCGCATCTACATGACC 180  
Db 165 GGGCTCTGGGTGTTCTGCTGCGCATGAGCAGATGAGAGCGGACCGCATCTACATGACC 224  
Qy 181 AACCTGGCGGTGGCGGCTCTGCTGCTGTGACCTTGTGCTTGTGCTGCTGCTGCTGCTGCTG 240  
Db 225 AACCTGGCGGTGGCGGCTCTGCTGCTGTGACCTTGTGCTTGTGCTGCTGCTGCTGCTGCTG 284  
Qy 241 CGAGACACTCAGACACACCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 300  
Db 285 CGAGACACTCAGACACACCGCTGTGCGAGCTCTCCAGGGCATCTACCTGACCAACAGG 344  
Qy 301 TACATGAGCATCAGCTGCTGATCAGGCCATGCGCGTGGAGCCGATATGTGGCCCTGGCGCAC 360  
Db 345 TACATGAGCATCAGCTGCTGATCAGGCCATGCGCGTGGAGCCGATATGTGGCCCTGGCGCAC 404  
Qy 361 CGGCTGCTGGTGGCGGCTGGGTCCCGCCAGCAGGCTGCGCGCGTGTGCGCGGTCTCTC 420  
Db 405 CGGCTGCTGGTGGCGGCTGGGTCCCGCCAGCAGGCTGCGCGCGTGTGCGCGGTCTCTC 464  
Qy 421 TGGGTGCTGGTTCATCGGCTCCCTGCTGGTCTGCTGGGTCTCTGGGATTCAGAGGCGCGC 480  
Db 465 TGGGTGCTGGTTCATCGGCTCCCTGCTGGTCTGCTGGGTCTCTGGGATTCAGAGGCGCGC 524  
Qy 481 TTCTGCTTCAGAGACACCGCGCAAAATTTCAATCTCATGCGGTTTCCCGTGTCTGGGATTC 540  
Db 525 TTCTGCTTCAGAGACACCGCGCAAAATTTCAATCTCATGCGGTTTCCCGTGTCTGGGATTC 584  
Qy 541 TACCTGCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTCCCTGGCCGAG 600  
Db 585 TACCTGCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAGGTGGTGAAGTCCCTGGCCGAG 644  
Qy 601 AGGCCACCCACAGCTGGGGCAGCAGAGGCCACCGCAAGGCTAAAGCATGCTCTGG 660  
Db 645 AGGCCACCCACAGCTGGGGCAGCAGAGGCCACCGCAAGGCTGCGCCGATGCTCTGG 704





Qy	781	ACCGAAGCTCTCAGATGCCAACTGTCGCTGGACGCCATCTGCTACTACTACATGGCC	840
Db	1356	ACCGAAGCTCTCAGATGCCAACTGTCGCTGGACGCCATCTGCTACTACTACATGGCC	1415
Qy	841	AAGGAGTTCAGGAGGCGTCTGCACTGGCGTGGCTCCCGTGCTAAGAGCCCAAAAAGC	900
Db	1416	AAGGAGTTCAGGAGGCGTCTGCACTGGCGTGGCTCCCGTGCTAAGAGCCCAAAAAGC	1475
Qy	901	CAGGACTCTCTGTGCGTGACCCCTCGCCTAA	930
Db	1476	CAGGACTCTCTGTGCGTGACCCCTCGCCTAA	1505

## RESULT 8

ADA84068  
ID ADA84068 standard; DNA: 1875 BP.

AC ADA84068:

DT 20-NOV-2003 (first entry)

Human GPR35 gene.

XX	human:	marker:	expressed	sequence	tag:	EST:	arabidopsis:	tumour:
----	--------	---------	-----------	----------	------	------	--------------	---------

KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

KW vaccine; ds; gene.

OS Homo sapiens.

PN WO2002103028-A2.

27-DEC-2002.

30-MAY-2002: 2002WO-IB004189.

PR 30-MAY-2001: 2001IIS-0293999P-XX

22-OCT-2001: 2001US-0330457P.  
PR

PR 19-FEB-2002; 2002US-0357144P.

PA (BIOM-) BIOMEDICAL CENT.

PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

AA  
DR  
WPI: 2003-175241/17.

DR P-PSDB; ADA84069.

Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.

PS Claim 23: Page 446-448: 516pp: English.

The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably *Arabidopsis* or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated antigen of the invention.





FT intron 3945. .5282  
 FT /tag= d  
 FT /number= 2  
 FT exon 5283. .5479  
 FT /tag= e  
 FT /number= 3  
 FT exon 5283. .5468  
 FT /tag= f  
 FT /number= 3\*  
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 FT intron 6619. .8372  
 FT /tag= j  
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 FT /tag= k  
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 FT intron 8515. .9009  
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 FT exon 9010. .9175  
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 FT 10619. .10784  
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 FT /tag= s  
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 FT intron 10988. .11146  
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 FT /tag= v  
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FT intron 11409. .12353  
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 FT exon 12354. .12553  
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 FT intron 30981. .31445  
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 FT /tag= af  
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 FT CDS 43070. .44944  
 FT /tag= ah  
 FT /note= "encodes GPR35 (AA79576)"  
 FT 44922. .44927  
 FT /tag= ai  
 FT polyA\_signal  
 FT WO200023603-A2.  
 PN 27-APR-2000.  
 PD 21-OCT-1999; 99WO-US024890.  
 PF 21-OCT-1998; 98US-0105052P.  
 PR 13-MAY-1999; 99US-0134175P.  
 PR (ARCH-) ARCH DEV CORP.  
 PA (TEXA ) UNIV OF TEXAS SYSTEM.  
 PA Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
 PI Hanis CL, Bell GI, Cox NJ;  
 PI WPI; 2000-339702/29.  
 DR P-PSDB; AA79567, AA79568, AA79569, AA79570, AA79571, AA79572,  
 DR AA79573, AA79574, AA79576.  
 XX Method for screening for type 2 diabetes mellitus comprises detecting a  
 FT polymorphism in a calpain encoding nucleic acid segment or a protease-  
 FT encoding nucleic acid segment.  
 FT  
 FT Claim 65; Page 203-217; 257pp; English.  
 PS  
 XX The present sequence is that of a 49,136 bp region located within the  
 CC NIDDM1 region of human chromosome 2. It includes the CAPN10 gene that  
 CC encodes a novel calpain-like cysteine protease, designated calpain 10,  
 CC and a gene encoding a G protein coupled receptor, GPR35. Alternative  
 CC splicing of calpain 10 mRNA generates a family of proteins. Isoforms 10a-  
 CC h (see AA79567-74) are respectively encoded by exons 1-7, 9-13, 1-  
 CC 7, 9, 10\*, 11-13, 1-7, 11-13, 1-7, 9, 11-13, 1-10\*, 11-13, 1-3\*, 4-7, 9-13,  
 CC 1, 2, 14, 15 and 1, 11-13. Calpain 10 mRNA is ubiquitously expressed; the  
 CC major 2.7 kb transcript was detected in every human adult and foetal  
 CC tissue examined. Mutations in the CAPN10 gene are responsible for









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Db      874  GGGCAACCTCTCGTGGTTCGGTCTGCTTCTGCTGCCCTGCACGTGGGGCTGACAGTGC 933
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Qy      779  TAACACAGCAAGCTCTCAGATGCCAACTGCTGCTGGAGCCCATCTGCTACTACTACATGG 838
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Db      1054  CCAAGGAGTTCAGGAGGCGTCTGCACTGGCGGTGGCTCCCGTGTAAAGGCCCAAAAA 1113
Qy      899  GCCAGGACTCTCTGCGGTGACCCCTCGCCTAA 930
Db      1114  GCCAGGACTCTCTGCGGTGACCCCTCGCCTAA 1145

RESULT 15
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ID  ADP28534 standard; DNA; 858 BP.
XX
AC  ADP28534;
XX
DT  12-AUG-2004 (first entry)
XX
DE  Human secreted protein encoding sequence SEQ ID #532.
XX
KW  Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW  cancer; inflammatory; immune; ds; human secreted protein.
XX
OS  Homo sapiens.
XX
PN  WO2004035732-A2.
XX
PD  29-APR-2004.
XX
PF  28-AUG-2003; 2003WO-US026780.
XX
PR  29-AUG-2002; 2002US-0406576P.
PR  29-AUG-2002; 2002US-0406579P.
PR  29-AUG-2002; 2002US-0406585P.
PR  29-AUG-2002; 2002US-0406588P.
PR  29-AUG-2002; 2002US-0406608P.
PR  29-AUG-2002; 2002US-0406611P.
PR  29-AUG-2002; 2002US-0406612P.
PR  29-AUG-2002; 2002US-0406616P.
PR  29-AUG-2002; 2002US-0406640P.
PR  29-AUG-2002; 2002US-0406642P.
PR  29-AUG-2002; 2002US-0406646P.
PR  29-AUG-2002; 2002US-0406653P.
PR  29-AUG-2002; 2002US-0406659P.
PR  29-AUG-2002; 2002US-0406666P.
PR  17-SEP-2002; 2002US-0410946P.
PR  17-SEP-2002; 2002US-0410947P.
PR  17-SEP-2002; 2002US-0410948P.
PR  17-SEP-2002; 2002US-0410949P.
PR  17-SEP-2002; 2002US-0410953P.
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PR  17-SEP-2002; 2002US-0410961P.
PR  17-SEP-2002; 2002US-0410962P.
PR  17-SEP-2002; 2002US-0411019P.
PR  17-SEP-2002; 2002US-0411022P.
PR  17-SEP-2002; 2002US-0411023P.
PR  17-SEP-2002; 2002US-0411024P.
PR  17-SEP-2002; 2002US-0411032P.
PR  17-SEP-2002; 2002US-0411035P.
PR  17-SEP-2002; 2002US-0411037P.
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PR  17-SEP-2002; 2002US-0411041P.
PR  17-SEP-2002; 2002US-0411045P.
PR  17-SEP-2002; 2002US-0411046P.
PR  17-SEP-2002; 2002US-0411048P.
PR  17-SEP-2002; 2002US-0411052P.
PR  17-SEP-2002; 2002US-0411055P.
PR  17-SEP-2002; 2002US-0411073P.
PR  17-SEP-2002; 2002US-0411082P.
PR  17-SEP-2002; 2002US-0411101P.
PR  17-SEP-2002; 2002US-0411111P.
PR  18-APR-2003; 2003US-0463700P.
PR  18-APR-2003; 2003US-0463708P.
PR  18-APR-2003; 2003US-0463716P.
PR  18-APR-2003; 2003US-0463732P.
PR  02-MAY-2003; 2003US-0467199P.
PR  02-MAY-2003; 2003US-0467201P.
PR  02-MAY-2003; 2003US-0467203P.
PR  02-MAY-2003; 2003US-0467230P.
PR  19-MAY-2003; 2003US-0471306P.
PR  19-MAY-2003; 2003US-0471338P.
PR  22-MAY-2003; 2003US-0472420P.
PR  22-MAY-2003; 2003US-0472430P.
PR  09-JUN-2003; 2003US-0476609P.
PR  09-JUN-2003; 2003US-0476641P.
PR  08-JUL-2003; 2003US-0485218P.
PR  08-JUL-2003; 2003US-0485223P.
PR  08-JUL-2003; 2003US-0485224P.
PR  08-JUL-2003; 2003US-0485325P.
PR  14-JUL-2003; 2003US-0486446P.
PR  14-JUL-2003; 2003US-0486480P.
PR  15-JUL-2003; 2003US-0486891P.
PR  15-JUL-2003; 2003US-0486960P.
PR  08-AUG-2003; 2003US-0493341P.
PR  08-AUG-2003; 2003US-0493370P.
PR  08-AUG-2003; 2003US-0493573P.
PR  08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
XX such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
XX genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 532; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
XX encoding a polypeptide which is believed to be cytostatic,
XX antiinflammatory, immunosuppressive, antibacterial and virucidal. The
XX composition and methods are useful for diagnosing, preventing and
XX treating diseases such as proliferative (e.g. cancer), inflammatory,
XX immune, metabolic, genetic, bacterial and viral diseases. The present
XX sequence represents a human secreted protein encoding sequence. The
XX present sequence is available on WIPWEB and is not in the specification.
XX
XX Sequence 858 BP; 125 A; 301 C; 260 G; 172 T; 0 U; 0 Other;
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Query Match 90.1%; Score 838; DB 12; Length 858;
Best Local Similarity 99.2%; Pred. No. 4,5e-158;
Matches 853; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
Qy 1 ATGAATGGCACCCTACAACACCTGTGGCTCCAGCGACCTCACTGCGCCCGCCAGCGATCAAG 60
Db 1 ATGAATGGCACCCTACAACACCTGTGGCTCCAGCGACCTCACTGCGCCCGCCAGCGATCAAG 60
Qy 61 CTGGGCTTCTAGCCCTACTTGGGCGCTCTGCTGGTGGCTAGGCTGCTGCTCAACAGCTTG 120
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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9: gb\_pr:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	922	99.1	169391	2	AC111190	AC111190 Homo sapi
5	920.4	99.0	930	9	AY275467	AY275467 Homo sapi
6	920.4	99.0	930	9	CR541765	CR541765 Homo sapi
7	920.4	99.0	1875	6	AR153299	AR153299 Sequence
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11	920.4	99.0	49136	6	AR153289	AR153289 Sequence
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## ALIGNMENTS

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DEFINITION	AX549206					
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VERSION	AX549206.1					
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SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	1	Burmer,G.C., Roush,C.L. and Brown,J.P.				
AUTHORS	Antigenic peptides, such as for G protein-coupled receptors					
TITLE	(GPCRs), antibodies thereto, and systems for identifying such					
JOURNAL	antigenic peptides					
FEATURES	Patent: WO 02061087-A 491 08-AUG-2002;					
source	Lifespan Biosciences, Inc. (US)					
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Best Local Similarity	99.7%;	Pred. No. 2.6e-136;				
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QY	61	CTGGGCTTCTAGCCTTCTGGGCTCTGGTGTAGGCTCTGCTCAACAGCCTG	120			
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QY	121	GGCTCTGGGTGTTCTGCTGGCGATGCGAGAGACCGGATCTTACATGACC	180			
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DEFINITION
ACCESSION AY275467
VERSION AY275467.1 GI:30526187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Warren,C.N., Aronstam,R.S. and Sharma,S.V.
TITLE Isolation of complete coding sequence for G-protein coupled
receptor 35 (GPR35)
JOURNAL Unpublished
2 (bases 1 to 930)
Warren,C.N., Aronstam,R.S. and Sharma,S.V.
REFERENCE Direct Submission
AUTHORS Submitted (11-APR-2003) Guthrie cDNA Resource Center, Guthrie
TITLE Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
JOURNAL Location/Qualifiers
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Best Local Similarity 99.4%; Pred. No. 1.5e-135;
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DEFINITION gene GPR35, G protein-coupled receptor 35; complete cds, incl.
stopcodon.
ACCESSION CR541765
VERSION CR541765.1 GI:49456486
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.
TITLE Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)
JOURNAL Unpublished
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COMMENT On Apr 22, 2002 this sequence version replaced gi:12313882.

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		/replace="g"	
		4533..4534	
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		/replace="cgggcaggccctgctg"	
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variation		/gene="RNPEPL1"	
		/replace="c"	
		4775..4891	
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		5113..5348	
exon		/gene="RNPEPL1"	
		/number=5	

RESULT 12

AF158748

LOCUS AF158748 Homo sapiens map 2q37.3, genomic sequence.

DEFINITION AF158748

ACCESSION AF158748.3 GI:20260805

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 65674)

AUTHORS Horikawa, Y., Oda, N., Cox, N.J., Li, X., Orho-Melander, M., Hara, M., Hinokio, Y., Lindner, T.H., Mashima, H., Schwarz, P., del Bosque Plata, L., Horikawa, Y., Oda, Y., Yoshiuchi, I., Colilla, S., Polonsky, K.S., Wei, S., Concannon, P., Iwasaki, N., Schulze, J., Baier, L.J., Bogardus, C., Groop, L., Boerwinkle, E., Hanis, C.L. and Bell, G.I.

TITLE Genetic variation in the gene encoding calpain-10 is associated with type 2 diabetes mellitus

JOURNAL Nat. Genet. 26 (2), 163-175 (2000)

MEDLINE 20472315

PUBMED 11017071

REFERENCE 2 (bases 1 to 65674)

AUTHORS Horikawa, Y.

TITLE Direct Submission

JOURNAL Submitted (17-MAR-1999) The University of Chicago, Howard Hughes Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago, Illinois 60637, USA

REFERENCE 3 (bases 1 to 65674)

AUTHORS Horikawa, Y.

TITLE Direct Submission

JOURNAL Submitted (19-JAN-2001) The University of Chicago, Howard Hughes Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago, Illinois 60637, USA

REMARK Sequence update by submitter

REFERENCE 4 (bases 1 to 65674)

AUTHORS Horikawa, Y.

TITLE Direct Submission

JOURNAL Submitted (22-APR-2002) The University of Chicago, Howard Hughes Medical Institute, 5841 S. Maryland Avenue MC1028, Chicago, Illinois 60637, USA

REMARK Sequence update by submitter



QY 841 AAGGAGTTCAGGAGCGTCTCACTGGCCGTGGCTCCCGGTCTAAGGCCCAAAAGC 900  
 |||||  
 Db 61023 AAGGAGTTCAGGAGCGTCTCACTGGCCGTGGCTCCCGGTCTAAGGCCCAAAAGC 61082  
 |||||  
 QY 901 CAGGACTCTCTGTGGTGCACCTCCGCTAA 930  
 |||||  
 Db 61083 CAGGACTCTCTGTGGTGCACCTCCGCTAA 61112  
 |||||

RESULT 13  
 AC124862/c  
 LOCUS Homo sapiens BAC clone RP11-27M15 from 2, complete sequence.  
 DEFINITION AC124862 AC080022  
 ACCESSION  
 VERSION AC124862.4 GI:22758809  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 160111)  
 Sultston,J.E. and Waterston,R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99063792  
 PUBMED 9847074

REFERENCE 2 (bases 1 to 160111)  
 AUTHORS Trani,L., Haakenson,W. and Schatzkammer,K.  
 TITLE The sequence of Homo sapiens BAC clone RP11-27M15  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-AUG-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 5 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 160111)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 REFERENCE 7 (bases 1 to 160111)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 COMMENT On Sep 8, 2002 this sequence version replaced gi:22091410.

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: sapiens@wustl.edu  
 ----- Summary Statistics  
 Center project name: H\_NH0027M15  
 Drafting Center: WIBR  
 -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is not the entire insert of the clone. This clone is overlapped by AC011298 and AC110619.

A transposon was identified in the finished region of this clone and removed prior to submission. The transposon would insert after base pair 85233 of this sequence.

The region from 21167 to 21405 was derived from a PCR product of project DNA.

The region from 107532 to 107628 was derived from a PCR product of project DNA.

The region from 126169 to 126182 was derived from a PCR product of project DNA.

The region from 126366 to 126648 was derived from a PCR product of project DNA.

Polymorphisms have been identified between AC108015, AC111190 and this sequence.

Data from AC108015 and AC111190 was used to finish this clone.

The sequence of AC080022 has been incorporated into AC124862.

#### FEATURES

Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="2"  
 /map="2"  
 /clone="RP11-27M15"  
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 297..563  
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 2200..2577  
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 7636..7940  
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 8960..9540  
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 10400..10441  
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 10769..10932  
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Qy	841	AAGGATTCACAGAGCGCTGTGCACATGGCGTGGCTCCCGCTGCTAAGGCCCAAAAGC	3411
Db	3352	AAGGATTCACAGAGCGCTGTGCACATGGCGTGGCTCCCGCTGCTAAGGCCCAAAAGC	3411
Qy	901	CAGGACTCTCTGTGCGTGACCCCTCGCCTAA	930
Db	3412	CAGGACTCTCTGTGCGTGACCCCTCGCCTAA	3441
RESULT 15			
ACCESSION	AK131540	3811 bp	mrna
LOCUS	AK131540		
DEFINITION	Homo sapiens cDNA FLJ16773 fis, clone BRAWH3046240, highly similar to Probable G protein-coupled receptor GPR35.		
KEYWORDS	AK131540.1 GI:470777595		
ORIGIN	oligo capping; fis (full insert sequence).		
REFERENCE	Homo sapiens (human)		
AUTHORS	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1		
REFERENCE	Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Tsuno, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamauchi, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuna, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masubo, Y., Nagai, K. and Isogai, T.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	2 (bases 1 to 3811)		
REFERENCE	Isogai, T. and Yamamoto, J.		
AUTHORS	Direct Submission		
TITLE	Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7		
JOURNAL	Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan		
COMMENT	(E-mail:genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: Reverse Proteomics Research Institute, HRI and RAB.		
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source	1. .3811		
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	/tissue_type="brain"		
	/clone_lib="BRAWH3"		
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	/note="unnamed protein product"		
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	/protein_id="BAD18676.1"		
	/db_xref="GI:47077596"		
	/translations="MTAGRSORRAEMGRSGVQGLDKGLDEFFFTAPMLSLRSFVFGVSGTSSHPAORNAEQCLAPARSLITSGSLCCPPTMTNGTYNTCCSSDLTWPPIAIKGGYALGVGLVLGLLNSLAWVFCRCMQQTETRIYNTNLAVADLCLTCLTPFVHLSRDTSPICQJLSQGIYLTNRNYSLSLTAIVADRYAVRHPLRAGRLSPRQRAAVCAVLWLVIGSLVARNMLLGGEGFCFSTRHNFNSMAFPFLGYLEPLAVVVFCAKVTALAQRPPTDVGQATRAKAMWANLVFVFCFLPHVGLTVRLAVGNACALLLSMIRRALYITSKLSANDCCLDIAICYYVMAXEFAQASALAVAPRAKAHKSQDSLCVTLA"		
ORIGIN			
Query Match	98.6%; Score 917.2; DB 9; Length 3811;		
Best Local Similarity	99.1%; Pred. No. 3.7e-135;		

Matches 922; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
Qy 1	ATGAATGGCACTACAAACACCTGTGGCTCCAGCGACCTCACTGTGCCCCCGAGCGATCAAG 60
Db	
2512	ATGAATGGCACTACAAACACCTGTGGCTCCAGCGACCTCACTGTGCCCCCGAGCGATCAAG 2571
Qy	61 CTGGGCTTCTACGCCCTACTTGGGGCTCTGTGGTGTAGGCTGCTGCTCAACAGCCTG 120
Db	
2572	CTGGGCTTCTACGCCCTACTTGGGGCTCTGTGGTGTAGGCTGCTGCTCAACAGCCTG 2631
Qy	121 GCGCTCTGGGTGTTCTGTGCGCATGCAGCAGTGGACGGAGACCCGCACTTACATGACC 180
Db	
2632	GCGCTCTGGGTGTTCTGTGCGCATGCAGCAGTGGACGGAGACCCGCACTTACATGACC 2691
Qy	181 AACCTGGCGGTGGCGCACTCTGCCCTGTGTGACCTTGGCCCTTGGTGTGCACTCCCTG 240
Db	
2692	AACCTGGCGGTGGCGCACTCTGCCCTGTGTGACCTTGGCCCTTGGTGTGCACTCCCTG 2751
Qy	241 CGAGACCTCAGACACGCCGCTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300
Db	
2752	CGAGACCTCAGACACGCCGCTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG 2811
Qy	301 TACATGACATCAGCCTCGTCAACGCCCATCGCCGTGACCCGCTATGTGCCCCGTGCGGCAC 360
Db	
2812	TACATGACATCAGCCTCGTCAACGCCCATCGCCGTGACCCGCTATGTGCCCCGTGCGGCAC 2871
Qy	361 CCGTGTGCTGCCCGCGGCTGCGGTCCCCAGGAGGCTGCGGCCGCTGTGCGCGGTCTCTC 420
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2872	CCGTGTGCTGCCCGCGGCTGCGGTCCCCAGGAGGCTGCGGCCGCTGTGCGCGGTCTCTC 2931
Qy	421 TGGGTGCTGGTTCATCGGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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2932	TGGGTGCTGGTTCATCGGCTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2991
Qy	481 TTCTGTCTTCAAGAGCACCGGCACAAATTTCAACTCCATGCGGTCCCGCTGCTGGGATTC 540
Db	
2992	TTCTGTCTTCAAGAGCACCGGCACAAATTTCAACTCCATGCGGTCCCGCTGCTGGGATTC 3051
Qy	541 TACCTGCCCCCTGGCGTGGTGTCTTCTGTCTCCCTGAAGGTGGTGACTGCCCTGGCCCCAG 600
Db	
3052	TACCTGCCCCCTGGCGTGGTGTCTTCTGTCTCCCTGAAGGTGGTGACTGCCCTGGCCCCAG 3111
Qy	601 AGGCCACCCACCGAGCTGGGGCAGGACAGGCCACCCGCAAGGCTAAACGCATGCTCTGG 660
Db	
3112	AGGCCACCCACCGAGCTGGGGCAGGACAGGCCACCCGCAAGGCTAAACGCATGCTCTGG 3171
Qy	661 GCCAACCTCCTGGTGTCTGTGGTCTGTCTTCTGTCCCTGCACTGGGGCTGACAGTGGCG 720
Db	
3172	GCCAACTCCTGGTGTCTGTGGTCTGTCTTCTGTCCCTGCACTGGGGCTGACAGTGGCG 3231
Qy	721 CTCGCAGTGGGCTGGAACGCCCTGTGCCCTCTCGAGAGCATCCGTCGCGCCCTGTACATA 780
Db	
3232	CTTGCAGTGGGCTGGAACGCCCTGTGCCCTCTCGAGAGCATCCGTCGCGCCCTGTACATA 3291
Qy	781 ACCAGCAAGCTCTAGATGCCAACTGTGCTGCTGGAGCGGCATCTGCTACTACATGGCC 840
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Db	
3352	AAGGAGTTCAGAGGCGCTGTGCACTGGCGCTGCTCCCGTGTAAAGGCCACAAAGC 3411
Qy	901 CAGGACTCTCTGTGGTGACCCCTCGCCTAA 930
Db	
3412	CAGGACTCTCTGTGGTGACCCCTCGCCTAA 3441

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:15:00 ; Search time 17 Seconds  
(without alignments)  
1748.881 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTCGSSDLTWPPAIAK.....AVAPRAKAHKSQSLCVTLA 309

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	24.8	370	JC5549	heptahelical P2Y5-
2	368.5	22.8	308	I50241	G protein-coupled
3	368.5	22.8	387	I82022	G protein-coupled
4	360.5	22.3	344	T09508	intron 17 purinerg
5	319	19.8	328	I54550	G protein-coupled
6	319	19.8	373	A47556	ATP receptor P2u -
7	318	19.7	362	S33733	G protein-coupled
8	315.5	19.5	365	S68679	G protein-coupled
9	312.5	19.4	364	JQ1488	bradykinin B2 rece
10	312.5	19.4	366	1 OORTB2	bradykinin recepto
11	310	19.2	342	S13638	platelet-activatin
12	308.5	19.1	375	A54946	P-2U nucleotide re
13	305.5	18.9	354	I53033	G protein-coupled
14	305.5	18.9	362	A57641	G protein-coupled
15	305	18.9	352	S60024	bradykinin B1 rece
16	304	18.8	342	A40191	platelet-activatin
17	302.5	18.7	362	B57641	G protein-coupled
18	302.5	18.7	373	JC4162	P2Y receptor - bov
19	301.5	18.7	362	S68207	G protein-coupled
20	298.5	18.5	373	JC4737	G protein-coupled
21	293	18.2	341	S43252	platelet-activatin
22	291	18.0	328	JC4800	P2Y6 receptor - hu
23	289	17.9	363	JC2543	angiotensin II rec
24	288.5	17.9	352	A43113	chemokine (C-C) re
25	285.5	17.7	361	B45680	G protein-coupled
26	283	17.5	341	S63666	platelet activatin
27	281.5	17.4	366	2 I49519	bradykinin B2 rece
28	279.5	17.3	363	2 I57955	somatostatin recep
29	279.5	17.3	364	2 JN0763	somatostatin recep

30	278	17.2	363	2 A49092	angiotensin II rec
31	276.5	17.1	361	2 JC5653	G protein-coupled
32	275	17.0	363	2 I48261	angiotensin II rec
33	275	17.0	363	2 I57940	somatostatin recep
34	272.5	16.9	355	2 I49339	macrophage inflam
35	271.5	16.8	420	2 I51667	thrombin receptor
36	271	16.8	354	2 T09353	G protein-coupled
37	269.5	16.7	365	2 S68208	G protein-coupled
38	269	16.7	323	1 Q0BED3	HHRF3 protein - hu
39	268	16.6	418	2 A46226	somatostatin recep
40	266.5	16.5	355	2 JC5067	G protein-coupled
41	263.5	16.3	369	2 JC5068	G protein-coupled
42	262.5	16.3	355	2 A45177	chemokine (C-C) re
43	262.5	16.3	391	2 A41795	somatostatin recep
44	262.5	16.3	391	2 C41795	somatostatin recep
45	262.5	16.3	391	2 A39297	somatostatin recep

ALIGNMENTS

RESULT 1

JC5549  
heptahelical P2Y5-like receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5549  
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.  
Biochem. Biophys. Res. Commun. 236, 106-112, 1997

A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.  
A:Reference number: JC5549; MUID:97366605; PMID:9223435  
A:Accession: JC5549  
A:Molecule type: DNA  
A:Residues: 1-370 <JAN>

C:Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB6322.1; PID:g2240034  
C:Superfamily: ATP receptor P2u  
Query Match 24.8%; Score 401; DB 2; Length 370;  
Best Local Similarity 34.0%; Pred. No. 2.7e-29;  
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

Qy	25	AYLGVLVLGILLNSLALWFCRCMQWTEIRYMTNLAVADLCCLCTLPF-VLHSLR---	81
Db	44	AVYSVVFILGHTNVSLSVFCFRMKRSETAIFTNLAVSLLFVCTLPFKIFYNPNRH	103
Qy	82	-DTSPTLQCLSQGIYLTNRVMSISLTAIAVDYVAVRHPLRARGLRSPQAAAVCAVL	140
Db	104	WPFQGT-LCKISGTAFLTNVGSMLFLTCISVDRELAIVYPRSTIITRRNSAIVCAGV	162
Qy	141	WVLVIGSLVARWLLGIOEGGF-----CFR-----STRHFNFSMRPFLLGFFYL	182
Db	163	WILVLSG-----GISASLFSTTNVNNATTCFEGLSKRVWKTYLSKITIPIEVVGFTI	215
Qy	193	PLAVVVFCSLKVVTAIAORPTDVCQAEAT-RKAARMWANLLVVFVCFPLHVGITVRL	241
Db	216	PLILNVSCSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMVAVFCVPVNSVFLYA	273
Qy	242	AVGNWAC--ALLEITIRALY-ITSKLSDANCCLDIAICYVMYMAKEFQESALAVAPRAKAH	298
Db	274	LVRSQATNCFERPAKIMYPITLCLATLNCDFDPFIYFTLTLESFQKSFYI-----NAH	327
Qy	299	KSQDSLQVLT 307	
Db	328	IRMESLPKT 336	

RESULT 2

I50241  
G protein-coupled receptor 6H1 - chicken  
N:Alternate names: purinoceptor 6H1  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50241; JC4618

R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
J. Immunol. 151, 628-636, 1993  
A;Title: Identification of a G protein coupled receptor induced in activated T cells.  
A;Reference number: 150241; MUID:93329058; PMID:8393036  
A;Accession: I50241  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-308 <KAP>  
A;Cross-references: UNIPROT:P32250; GB:I06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.  
Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
A;Reference number: JC4618; MUID:96190677; PMID:8619790  
A;Accession: JC4618  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-308 <WEB>  
A;Cross-references: GB:I06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
A;Experimental source: T-cells  
C;Comment: This receptor plays a role in T-cell activation.  
C;Genetics:  
A;Gene: P2Y5  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein  
F;15-40/Domain: transmembrane #status predicted <TM1>  
F;51-74/Domain: transmembrane #status predicted <TM2>  
F;89-109/Domain: transmembrane #status predicted <TM3>  
F;133-153/Domain: transmembrane #status predicted <TM4>  
F;177-201/Domain: transmembrane #status predicted <TM5>  
F;227-248/Domain: transmembrane #status predicted <TM6>  
F;269-292/Domain: transmembrane #status predicted <TM7>  
Query Match 22.8%; Score 368.5; DB 2; Length 308;  
Best Local Similarity 30.3%; Pred. No. 2.2e-26;  
Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIIKLGFGY-AYLGVLVLLGLLNSIALWFCRCMQOWTETRIYMTNLAVADLC 68  
DB 3 SNNCTEDSFKTYLGCVFMSVFLGLIANCAVIFFTLKVRNETTYMLNLAISDLL 62  
QY 69 LLCTLPFVLSLRDSDTP-----LCQLSQGYLITRYMSISLVTAIVDRYVAVRHPLRA 124  
DB 63 FVFTLPFRIFYE-VVRNWPFGDVLCKISVTLFVNTMYGSIILFTLCISVDRFLAIVHPFS 121  
QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQEGGFCFRST-RHNFSMR-----FP- 176  
DB 122 KTLRTKRNARIVCAVWITVLAGSTPASF-----FQSTNRQNNTQRTCPENFPE 171  
QY 177 -----LLGFLPLAVVFGSLKVTALAQRPPTDVQGAETRAKAAVMWA 221  
DB 172 STWKTYLSRIVIFIEIVGFPIILNVTCTWVLRTL-NKPLTLRNKLSKKKVKMIFV 230  
QY 222 NLLVFWVCPPLHVGIL---TVRLAVGWNACALLETIRRALYITSKLSDANCCDAICYYY 278  
DB 231 HLVIFFCFVPVNIITLILYSLMRTQTWNCVVAVRTWYPVTLCTAVSNCCFDPVIVYF 290  
RESULT 3  
169202  
G protein-coupled receptor HM74 - human  
C;Species: Homo sapiens (man)  
C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I69202  
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.  
Int. Immunol. 5, 1239-1249, 1993  
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem  
A;Reference number: I54751; MUID:94092629; PMID:7505609  
A;Accession: I69202  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-387 <RES>  
A;Cross-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867  
C;Genetics:  
A;Gene: HM74

C;Superfamily: G protein-coupled receptor 4

Query Match 22.8%; Score 368.5; DB 2; Length 387;  
Best Local Similarity 34.3%; Pred. No. 2.8e-26;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;  
QY 27 LGVLLVLLGLLNSIALWFCRCMQOWTETRIYMTNLAVADLCCLCTLPFVL-----HSUR 81  
DB 34 LGLEFIFGLLNGLAWIFCFHLKSKSRFLFNLAVADFLIICLPVMDYVVRSDW 93  
QY 82 DTSPTPLCQLSQGYLITRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAACAVLW 141  
DB 94 NFGDIP-CRLVLFNFMNRQSGIIFLTIVVAVDRYVVRVHPHALNKISNWTAAIISCLIW 152  
QY 142 VLVIG---SIVARWLLGIQEGG---GFCFR-STRHNF---NSMRPFLGLFYLPLAVVVFCSLK 193  
DB 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLLPLGLIILFCSAR 210  
QY 194 VVTLAQRPPTDVQGAETRAKAAVMWANLLVFCFLPLHVLTVRLAVGW-----N 246  
DB 211 IILSLRQR---QMDHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFMLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCDAICYYYMAKEF 283  
DB 265 NCEVYRVDLAFFITLSFTYMNMLDPVYVYFSSPSF 301  
RESULT 4  
T09508  
Intron 17 purinergic receptor P2Y5 - human  
N;Alternate names: G-protein coupled receptor  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.  
submitted to the EMBL Data Library, April 1997  
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinol  
A;Reference number: Z16705  
A;Accession: T09508  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-344 <BOH>  
A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g23232068; PID:g23232069  
A;Map position: 13  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein  
Query Match 22.3%; Score 360.5; DB 2; Length 344;  
Best Local Similarity 29.2%; Pred. No. 1.3e-25;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIIKLGFGYAYL-GVLLVLLGLLNSIALWFCRCMQOWTETRIYMTNLAVADLC 68  
DB 6 SSHCFYNSDFKTYLGCVMFVFLVLSNCVAIVIFICVLKVRNETTYTMINLAISDLL 65  
QY 69 LLCTLPFVLSLRDSDTP-----LCQLSQGYLITRYMSISLVTAIVDRYVAVRHPLRA 124  
DB 66 FVFTLPFRIFYE-VVRNWPFGDVLCKISVTLFVNTMYGSIILFTLCISVDRFLAIVYF 124  
QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176  
DB 125 KTLRTKRNARIVCTGVNLTIGGSAPAVFVQSTHSGQNNASACFEN-----FPEA 175  
QY 177 -----LLGFLPLAVVFGSLKVTALAQRPPTDVQGAETRAKAAVMWA 221  
DB 176 TWKTYLSRIVIFIEIVGFPIILNVTCTWVLRTL-NKPLTLRNKLSKKKVKMIFV 233  
QY 222 NLLVFWVCPPLHVGIL---TVRLAVGWNACALLETIRRALYITSKLSDANCCDAICYYY 278  
DB 234 HLVIFFCFVPVNIITLILYSLMRTQTWNCVVAVRTWYPITLCTAVSNCCFDPVIVYF 293  
QY 279 MAKEFOEA 286

Qy	2	NGIYNTCGSSDLTWPPAIKLG----	YAYL-----	GVLLVLCILLNSIALWVFCR	48
Db	9	NSTINGTWEGD-----	ELGYKCRFNE	DFKIVLLPVSYGVVCLGCLNVALVYFLCR	61
Qy	49	MOOWTETRIYMTNLAVADLCILCTLPFLVHSLRDTSDTP-----	LCQLSGQIYLTNRYMSI	104	
Db	62	LKTWNASTTYMFLAVSDLSYAASIPLLVYYYARGDHWPFSTVLC	KVRLFYTNLYCSI	121	
Qy	105	SLVTAIAVDRYAVRHPLRAGLRSPQAAAVCAVLVVLVTGSLVARWMLLGIQEGGFCFR	164		
Db	122	LFLTCISVHRCLGVLRLPLHSLRWGRARYARVAAVWVVLVL--	ACQAPVLYFVTTSVRGTR	180	
Qy	165	STRIN-----	FNSMRPPLGLPYLPLAVVFCSLKVVTAALORPP--	TDVGOAE	210
Db	181	ITCHDTSARELFSHFVAYSVMVLGLL--PAVFPFVILVICYLMARRLL--	KPAYGTTGGPLPR	238	
Qy	211	ATRKAAARMWANLLVFVVCFLPHVGLTVRLAVGW--	NACALLETRRVALYITSKLS DAN	268	
Db	239	AKRKSVRTIALVLAVFALCPLPFHVHTRTYLTSFRSLDLSCHTLNAINMAYKITRPLASAN	298		
Qy	269	CCLDAICYYY-----	MAKEFQEASALAVAPRAK	296	
Db	299	SCLDPVLYFLAGQLRVRFARDAPKPTBETPSPQAR	333		
RESULT 7					
S33733					
G protein-coupled receptor - chicken					
C:Species: Gallus gallus (chicken)					
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004					
C:Accession: S33733					
R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F. FEBS Lett. 324, 219-225, 1993					
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP re					
A:Reference number: S33733; MUID:93285340; PMID:8508924					
A:Accession: S33733					
A>Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-362 <WEB>					
A:Cross-references: UNIPROT:P34996; ENBL:X73268; NID:G395084; PIDN:CAAS1716.1;					
C:Superfamily: ATP receptor P2u					
C:Keywords: G protein-coupled receptor; transmembrane protein					
Query Match 19.7%; Score 318; DB 2; Length 362;					
Best Local Similarity 28.2%; Pred. No. 1.2e-21;					
Matches 96; Conservative 63; Mismatches 13; Indels 48; Gaps 12					
Qy	1	MNGTY-----	NTCGSSDLTWPPAIKLG--	YAYLGVLLVL----	GLLNLSLALW 44
Db	10	LNNGTQPELLAGGWAAGNATTKCSLT-----	KTGFQFYLP	TVYILVFTIGFLGNSVAIWM	64
Qy	45	PCCRMQOWTETRIYMTNLAVADLCILCTLPFLVHSLRDTSD-----	TPCLCOLSGQIYLTNR	100	
Db	65	PVFHMRPWSGISVYMFNLALADFLVLTLPALIFYYFNKTDWI	FGDVNMCKLQRFIFHVNLL	124	
Qy	101	YMSISLVTAIADVRYAVRHPLRAGLRSPQAAAVCAVLVVLVTGSLVARWMLL----	GI	156	
Db	125	YGSILFLTCSVHRITYGVVHPLKSLGRKKXNAVYVSSLVWALVV--	AVIATPILFVSGTGV	183	
Qy	157	QEGG--	FCFSTRHNF-----	NSMRPPLGLGYLPLAVVFCSLKVVTAALORPPPTDVGO	208
Db	184	RRNKTIICYDTTADBYLRSYFVSMCTTVFMFCIPFIVILG	CYGLIVKALIKYK--	DLDN	240
Qy	209	AEATRKAAARMWANLLVFVVCFLPHVGLTVRLAVGWN-----	ACALLETRRVALYITSK	263	
Db	241	SPLRKRKSIYLIIVLTVFVSYLSPHVMKTLNLRDLDFQTPQMCAFNKDVKVYATQVTRG	300		
Qy	264	LSDANCLDLAICYYYMAKEFQEASALAVAPRAKAHKSQDSL	304		
Db	301	LASLNSCVDPLYFLAGDTFRR--	RLSRATRKSSRRSEPNV	339	



A:Residues: 1-366 <MCE>  
A:Cross-references: UNIPROT:P25023; GB:M59967  
R:Pesquero, J.B.; Lindsey, C.J.; Zen, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.  
J. Biol. Chem. 269, 26920-26925, 1994  
A:Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence  
A:Reference number: A55079; MUID:95014558; PMID:7929432  
A:Accession: A55079  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-75, 'A', 77-366 <PES>  
A:Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190  
R:Wang, D.; Ma, J.; Chao, L.; Chao, J.  
Biochim. Biophys. Acta 1219, 171-174, 1994  
A:Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.  
A:Reference number: S47529; MUID:94368850; PMID:8086459  
A:Accession: S47529  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-366 <WAN>  
A:Cross-references: EMBL:L26173; NID:9476749; PIDN:AAA62492.1; PID:9685244  
C:Comment: this G protein-coupled receptor binds the nonapeptide bradykinin.  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;  
F:31-48/Domain: transmembrane #status predicted <TM1>  
F:79-96/Domain: transmembrane #status predicted <TM2>  
F:107-126/Domain: transmembrane #status predicted <TM3>  
F:154-170/Domain: transmembrane #status predicted <TM4>  
F:197-215/Domain: transmembrane #status predicted <TM5>  
F:245-261/Domain: transmembrane #status predicted <TM6>  
F:3.14,182/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:105-186/Disulfide bonds: #status predicted  
F:326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.4%; Score 312.5; DB 1; Length 366;  
Best Local Similarity 28.1%; Pred. No. 3.8e-21;  
Matches 90; Conservative 54; Mismatches 127; Indels 49; Gaps 9;

QY 2 NGTYNTGSSDLTWPAKLGFGYAVLGVLLGLLNSLALWVFCRMOQWTETRIYMTN 61  
DB 14 NGTFSEVNCPTPEWMSWLNIAQAPLWFLFLAALENIFVLSVFLHKTINCTVABEYILGN 73  
QY 62 LAVADLCLLCTLPFVLSLRDTSF---TPLCOLSGIYLTNRYMSISLVTAIAVDRYVA 117  
DB 74 LAGADLLIACGLPFWAITIANNFDMFLGFEVLRVNTMYMLYSSICFLMLVSDIRYLA 133  
QY 118 VRHPLRARGLRSPROAAVCAVLW--LVVIGS--LVARWLLGIORGCGFCFRSTRN--- 169  
DB 134 LVKWTSMGMRGVRWAKLYSLVMSCTLLSSPMLVFTMKDYREG-----HNVTAAC 186  
QY 170 -----FNSMRFPLLGYPYLVAVVFCSLKVVTAIAQRPPTDVQQAETRAARM 218  
DB 187 VIVYPSRSWEVFTNMLNLVGLPLLSIITFTVRIMQVLRNEMKKFQVQTEKKATVL 246  
QY 219 VVANLLVFCVFLPHVG--LTVRLAVG-----WNAALLETIRALYITSKLSF---A 267  
DB 247 VLAVLGLFLVCFPPQISTFDTLLRLGLVSGCN-----EAVDIVTQISSYVAYS 298  
QY 268 NCCLDAICVYVMAKQFQAS 287  
DB 299 NSCLNPLVIVGKFRKKS 318

RESULT 11  
S13638  
platelet-activating factor receptor - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
A:Accession: S13638  
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, H.; To  
Nature 349, 342-346, 1991  
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu  
A:Reference number: S13638; MUID:91101726; PMID:1846231  
A:Accession: S13638

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-342 <HON>  
A:Cross-references: UNIPROT:P21556; GB:X56736; NID:949442; PIDN:CAA40060.1; PID:949443  
A:Note: the species of guinea pig is not identified; in GenBank entry CCDAFREC, release  
C:Superfamily: ATP receptor P2U

Query Match 19.2%; Score 310; DB 2; Length 342;  
Best Local Similarity 28.2%; Pred. No. 6e-21;  
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

QY 29 VLLVLGLLNSLALWVFCRMOQWTETRIYMTNLAVALDCLCTLP--FVLHSLRDT 83  
DB 24 IIFVLGIANGVLMVFP-ARLYPSKLNKIKFMVNLTVADLLFLITLPLWIVVYSGNQ 82  
QY 84 SDTP--LCOLSGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPROAAVCAVLW 141  
DB 83 WFLPKFLCNLAGCLFFINTYCSVAFVLGVTYNRFOAVKYPKTAQTATTKRGIALSLV 142  
QY 142 VLVTGSLVARWLLGQEQ-----GGFCFRSTRHNFNSMRPPL-----LGFYPLA 185  
DB 143 VAIVAA--ASYFLVMDSTNVVSNKAGSGNITRCFEHYEKGSKPVLIIHICIVLGF 200  
QY 186 VVVFCSLKVVTALAQRPPTDVQQAETRAKARMVWNLVVFVFCFLPLHVLTVRLAVGM 245  
DB 201 LILFCNLVLIHTLLRQPVKQORNAEVRRLMMVCTVLAVFVICFVPHHM-----VQLPW 255  
QY 246 NACAL-----LETIRALYITSKLSDCANCCDAICYYYMAKBFQE 285  
DB 256 TLAEIGMWPSSNHQAINDAHOVTLCLLSTNCVLDPIVFCFLTKFRK 302

RESULT 12  
A54946  
P-2U nucleotide receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1999  
A:Accession: A54946  
R:Par, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cysti-  
A:Reference number: A54946; MUID:94211846; PMID:8159738  
A:Accession: A54946  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-375 <PAR>  
A:Cross-references: GB:U07225  
A:Note: parts of this sequence were confirmed by protein sequencing  
C:Genetics:  
A:Gene: GDB:P2RY2; HP2U; P2U  
A:Cross-references: GDB:362713; OMIM:600041  
A:Map position: 11q13.5-11q14.1  
C:Superfamily: ATP receptor P2U  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 308.5; DB 2; Length 375;  
Best Local Similarity 31.7%; Pred. No. 9e-21;  
Matches 89; Conservative 41; Mismatches 104; Indels 47; Gaps 8;

QY 28 GVLVLGLLNSLALWVFCRMOQWTETRIYMTNLAVALDCLCTLPFVLHSLRDTSDTP 87  
DB 41 GWVCVLGLCNVAGLYIFLCRLKTNASTTYMFLHVASDALYAAASLPLVYYARGDHP 100  
QY 88 ---LCOLSGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPROAAVCAVLW 143  
DB 101 FSTVLCKLVRFYTNLYCSILFLTCISVHRCGLVRLRSLRWRGARYARRVAGAVWL 160  
QY 144 VIGSLVARWLLGIORGCGFCFRSTRHNFNSMRPPL-----LGF 180  
DB 161 V-----LACQAPVLYFVT-----SARGPLTCHDTSAPFLSRFVAYSSVMLGLLF 206  
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVQQAETRAKARMVWNLVVFVFCFLPLHVLGT 238

Db 207 AVPPAVILVYVLMARRLL-KPAYGTSGGLPRAKRSVRTIAVLAVFALCFLPFHVRT 265  
QY 239 VRLAVGW--NACALLETRIRALYITSKLSDANCCLDAICY 277  
Db 266 LYSFRLSDLSCHTLNAINMA-YKVTRLASANSCLDPVLYF 305

RESULT 13  
I53033  
G protein-coupled receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I53033  
R:Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, R.  
DNA Cell Biol. 14, 25-35, 1995  
A:Title: Isolation of three novel human genes encoding G protein-coupled receptors.  
A:Reference number: I53033; MUID:95134353; PMID:7832990  
A:Accession: I53033  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-354 <RES>  
A:Cross-references: UNIPROT:P46093; GB:I36148; NID:g598152; PIDN:AAA63180.1; PID:g598153  
C:Superfamily: G protein-coupled receptor 4  
C:Keywords: G protein-coupled receptor

Query Match 18.9%; Score 305.5; DB 2; Length 354;  
Best Local Similarity 31.0%; Pred. No. 1.6e-20;  
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWETRIY 58  
Db 3 NHTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLALWAAVYQVQRNELGY 55

QY 59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTFLCQLSQGIYLTNRYMSISLVTAIAVD 114  
Db 56 LMNLSIADLLYICTLPWVDYFLHNDNIHGPCKLFGFIYTYNIYISIAFLCCISVD 115

QY 115 YVAVRHLPLRARGLSRQAAACAVLWLVIGSLVARWLLGIEGQGFCSRST-RHNFSNM 173  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAVMW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVFPVCFPLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAVMW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVFPVCFPLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAVMW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVFPVCFPLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAVMW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVFPVCFPLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 228 SLIAIVLVCFAPYHVLLSRAIYLGRPWD-CGFEERVFSAHYHSSLAFTSLNCVADPILY 286

RESULT 14  
A57641  
G protein-coupled receptor 4 - human  
C:Species: Homo sapiens (man)  
C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: A57641  
R:Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.  
Genomics 30, 84-88, 1995  
A:Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome  
A:Reference number: A57641; MUID:96129306; PMID:8595909  
A:Accession: A57641  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-362 <MAH>  
A:Cross-references: UNIPROT:P46093; GB:U21051; NID:g687793; PIDN:AAA98457.1; PID:g687794  
C:Genetics:  
A:Gene: GDB:GPR4  
A:Cross-references: GDB:371710; OMIM:600551  
A:Map position: 19q13.3-19q13.3  
A:Introns: #status absent  
C:Superfamily: G protein-coupled receptor 4  
C:Keywords: G protein-coupled receptor

Query Match 18.9%; Score 305.5; DB 2; Length 362;  
Best Local Similarity 31.0%; Pred. No. 1.6e-20;  
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWETRIY 58  
Db 3 NHTWEGCHVDSRVDHLFPFSL-----YIFVIGV-GLPTNCLALWAAVYQVQRNELGY 55

QY 59 MTNLAVADLCLLCTLP-----FVLHSLRDTSDTFLCQLSQGIYLTNRYMSISLVTAIAVD 114  
Db 56 LMNLSIADLLYICTLPWVDYFLHNDNIHGPCKLFGFIYTYNIYISIAFLCCISVD 115

QY 115 YVAVRHLPLRARGLSRQAAACAVLWLVIGSLVARWLLGIEGQGFCSRST-RHNFSNM 173  
Db 116 YLAVAHPLRFARLRVKTAVASVVVWATELGANSAP--LFHDE--LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAVMW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVFPVCFPLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 228 SLIAIVLVCFAPYHVLLSRAIYLGRPWD-CGFEERVFSAHYHSSLAFTSLNCVADPILY 286

RESULT 15  
S60024  
Bradykinin B1 receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S60024  
R:MacNeil, T.; Bierilo, K.K.; Menke, J.G.; Hees, J.F.  
Biochim. Biophys. Acta 1264, 223-228, 1995  
A:Title: Cloning and pharmacological characterization of a rabbit bradykinin B(1) receptor  
A:Reference number: S60024; MUID:96085127; PMID:7495867  
A:Accession: S60024  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352 <MAC>  
A:Cross-references: UNIPROT:P48748; EMBL:U20507; NID:g1041820; PIDN:AAC48482.1; PID:g1041820  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.9%; Score 305; DB 2; Length 352;  
Best Local Similarity 26.6%; Pred. No. 1.8e-20;  
Matches 89; Conservative 62; Mismatches 131; Indels 52; Gaps 10;

QY 7 TCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWETRIYMTNLAVAD 66  
Db 24 SCGAPDAWDLHLRL-LPTFIIAIFTGLGNSFVLSVFLARRRLSVAEILANLAASD 82

QY 67 LCLLCTLPVHLSLRDTSDTP-----LCQLSQGIYLTNRYMSISLVTAIAVDRAVVRHPL 122  
Db 83 LVFVLGLFPWAEVNRNQDFWPFGAALCRVINGVIKANLFIISFLVVAISQDRYSVLVHPM 142

QY 123 RARGLSRQAAACAVLWLVIGSLVARWLLGIEGQGFCSRSTR-----167  
Db 143 ASRRGRRRQAQTALW--IAGGL-----LSTPTFVLSRVRAVPELVNSACILLPLP 193

QY 168 ----HNFNSMRPFLGFLPLAVVFCSLKVVTAL---AQRPTDVGQAEATRKAAVMW 220  
Db 194 HEAWHLRWELNLLGLFLPLAAILFFNCHILASLRRRGVRVPSRCGGPRDSKSTA-LIL 252

QY 221 ANLLVFPVCFPLPHVGLTVRL-----AVGWNACALLETRIRALYITSKLSDANCCLDAIC 275  
Db 253 TLVASFVLCWAPYHFFAFLECLWQVHAIG--CCFWEEFTDLGLQLSNFSAFVNSCLNPVI 310

QY 276 YYYMAKER-----QEASALAVAPRAKAKHSQ 301  
Db 311 YVFGRLFTKVKWELCQCQCSPLAPVSSRRKE 344

Search completed: May 23, 2005, 11:30:20

Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:07:54 ; Search time 63 Seconds  
(without alignments)  
1896.968 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKAHKSQSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614	100.0	309	3 AAY79576	Aay79576 Human G p
2	1614	100.0	309	5 ABG95159	Abg95159 Human GPC
3	1614	100.0	309	6 ABP82002	Abp82002 Human G p
4	1614	100.0	309	7 ADP867656	Adp867656 Human G p
5	1614	100.0	309	8 ADO29394	Ado29394 Human GPC
6	1614	100.0	309	8 ADO78094	Ado78094 Human GPC
7	1609	99.7	309	5 ABG95172	Abg95172 Human GPC
8	1608	99.6	309	3 AAY69989	Aay69989 Human rec
9	1608	99.6	547	7 ADF70461	Adf70461 Orphan re
10	1606	99.5	309	7 ADF50511	Adf50511 Human GPC
11	1602	99.3	309	3 AAY58645	Aay58645 Human G-p
12	1602	99.3	309	6 ADA84069	Ada84069 Human GPC
13	1602	99.3	394	8 ADO78095	Ado78095 Human GPR
14	1602	99.3	394	8 ADR10454	Adr10454 Human pro
15	1382	85.6	286	8 ADP29765	Adp29765 Human sec
16	1124	69.6	307	8 ADO29395	Ado29395 Mouse GPC
17	402	24.9	370	2 AAW62597	Aaw62597 Human 7-c
18	402	24.9	370	5 ABP61511	Abp61511 Human NF-
19	402	24.9	370	6 ABG73513	Abg73513 Human p2y
20	402	24.9	370	6 ABP81870	Abp81870 Human G p
21	402	24.9	370	7 ADH69286	Adh69286 Human pur
22	402	24.9	370	8 ADP91778	Adp91778 Human p2y
23	402	24.9	370	8 ADO29049	Ado29049 Human nov
24	402	24.9	370	8 ADQ88244	Adq88244 Human 241
25	402	24.9	370	8 ADQ81575	Adq81575 Human 1ys

26	402	24.9	608	7 ADF70491	Adf70491 Orphan re
27	401	24.8	370	7 ADH69285	Adh69285 Human pur
28	401	24.8	370	8 ADF91777	Adf91777 Human p2y
29	397	24.6	370	8 ADO29050	Ado29050 Mouse nov
30	392	24.3	370	5 ABP61510	Abp61510 Human NF-
31	385	23.9	327	8 ADO29415	Ado29415 Mouse GPC
32	376.5	23.3	363	5 AAU77993	Aau77993 Human inf
33	376.5	23.3	363	5 ADJ63782	Adj63782 Human G p
34	376.5	23.3	363	7 ADF28998	Adf28998 Human G p
35	376	23.3	319	2 AAY30313	Aay30313 AnMaid G
36	376	23.3	319	3 AAY79562	Aay79562 Human G p
37	376	23.3	319	8 ADH68205	Adh68205 Human G-p
38	376	23.3	319	8 ADR73578	Adr73578 Human var
39	376	23.3	383	4 ABG23843	Abg23843 Novel hum
40	376	23.3	557	7 ADF70422	Adf70422 Orphan re
41	375.5	23.3	362	6 ABG72358	Abg72358 Human orp
42	375.5	23.3	363	2 AAW94654	Aaw94654 G-protein
43	375.5	23.3	363	4 AAU04379	Aau04379 Human G-p
44	375.5	23.3	363	6 ABG72361	Abg72361 Rabbit or
45	375.5	23.3	363	7 ADC86215	Adc86215 Human GPC

ALIGNMENTS

RESULT 1  
AAY79576  
ID :AAY79576 standard; protein; 309 AA.  
XX  
AC AAY79576;  
XX  
DT 15-AUG-2000 (first entry)  
XX  
DE Human G protein coupled receptor GPR35.  
XX  
KW GPR35; G protein coupled receptor; human; NIDDM1;  
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
KW diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 174 /note= "encoded by GCG"  
FT Misc-difference 294 /note= "encoded by AGT"  
XX  
PN WO200023603-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 21-OCT-1999; 99WO-US024890.  
XX  
PR 21-OCT-1998; 98US-0105052P.  
PR 13-MAY-1999; 99US-0134175P.  
XX  
(ARCH-) ARCH DEV CORP.  
XX (TEXA ) UNIV OF TEXAS SYSTEM.  
XX  
PI Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
PI Hanis CL, Bell GI, Cox NJ;  
XX  
DR WPI: 2000-339702/29.  
DR N-PSDB; AAA27485, AAY79574, AAY79576.  
XX  
PT Method for screening for type 2 diabetes mellitus comprises detecting a  
PT polymorphism in a calpain encoding nucleic acid segment or a protease-  
PT encoding nucleic acid segment.  
XX  
PS Claim 75; Page 237-238; 257pp; English.  
XX  
CC The present sequence is that of the human gene encoding G protein coupled  
CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The

CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
 CC (34.1% identity) suggesting that ATP or other nucleotide is its ligand.  
 CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
 CC relatively higher levels in adult lung, small intestine, colon and  
 CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
 CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
 CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
 CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10  
 CC gene, which encodes a novel calpain-like cysteine protease, designated  
 CC calpain 10. Mutations in the CAPN10 gene are responsible for a  
 CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
 CC propensity for type 2 diabetes mellitus are based on detection of a  
 CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
 CC for identifying modulators of calpain activity, and using these  
 CC modulators to treat diabetes, in particular through the regulation of an  
 CC insulin secretory response or insulin mediated glucose transport  
 XX

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 3; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
 DB |||||  
 QY 1 MNGTYNTCGSSDLTPPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
 DB |||||  
 QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSGIYLTNRVMSISLVTIAVDRYVAVRH 120  
 DB |||||  
 QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSGIYLTNRVMSISLVTIAVDRYVAVRH 120  
 DB |||||  
 QY 121 PLRAGRLSPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTHNFNSMRPPLGFG 180  
 DB |||||  
 QY 121 PLRAGRLSPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTHNFNSMRPPLGFG 180  
 DB |||||  
 QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVGQAEATKKAARMWVWVLLFVVCFLPHVGLTVR 240  
 DB |||||  
 QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVGQAEATKKAARMWVWVLLFVVCFLPHVGLTVR 240  
 DB |||||  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKQFQASALAVAPRAKAHKS 300  
 DB |||||  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKQFQASALAVAPRAKAHKS 300  
 DB |||||  
 QY 301 QDSLVCVTILA 309  
 DB |||||  
 QY 301 QDSLVCVTILA 309

RESULT 2  
 ABG95159  
 ID ABG95159 standard; protein; 309 AA.  
 AC ABG95159;  
 XX  
 DT 04-DEC-2002 (first entry)  
 DE Human GPCR GPR35.

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
 KW hypertension; reflux disease; depression, migraine; schizophrenia; ulcer;  
 KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
 KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
 KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 KW prostatic hypertrophy; receptor.

XX Homo sapiens.  
 OS  
 XX WO200268600-A2.  
 PN  
 XX 06-SEP-2002.  
 PD  
 XX 26-FEB-2002; 2002WO-US005625.  
 PF  
 XX

PR 26-FEB-2001; 2001US-0271913P.  
 XX (AREN-) ARENA PHARM INC.  
 PA  
 XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX WPI; 2002-706980/76.  
 DR N-PSDB; ABS73345.  
 XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
 PT or inverse agonist compounds for treating diseases associated with GPCR.  
 PT  
 XX Claim 29; Page 128-130; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic,  
 CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents an endogenous human GPCR

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 5; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
 DB |||||  
 QY 1 MNGTYNTCGSSDLTPPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRQMQWTETRIYMT 60  
 DB |||||  
 QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSGIYLTNRVMSISLVTIAVDRYVAVRH 120  
 DB |||||  
 QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSGIYLTNRVMSISLVTIAVDRYVAVRH 120  
 DB |||||  
 QY 121 PLRAGRLSPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTHNFNSMRPPLGFG 180  
 DB |||||  
 QY 121 PLRAGRLSPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTHNFNSMRPPLGFG 180  
 DB |||||  
 QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVGQAEATKKAARMWVWVLLFVVCFLPHVGLTVR 240  
 DB |||||  
 QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVGQAEATKKAARMWVWVLLFVVCFLPHVGLTVR 240  
 DB |||||  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKQFQASALAVAPRAKAHKS 300  
 DB |||||  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKQFQASALAVAPRAKAHKS 300  
 DB |||||  
 QY 301 QDSLVCVTILA 309  
 DB |||||  
 QY 301 QDSLVCVTILA 309

RESULT 3  
 ABP82002  
 ID ABP82002 standard; protein; 309 AA.  
 XX  
 AC ABP82002;  
 XX  
 DT 04-MAR-2003 (first entry)  
 DE Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;



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Db 121 PLRAGLSRQAAAVCAVLVWLVIGSLVARWLLGQGGFCFSTRFNSMRPFLG 180
QY 181 YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAARMWVANLLVFVVCFLPLHGLTVR 240
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAARMWVANLLVFVVCFLPLHGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAKHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAKHS 300
QY 301 QDSLVCVTLA 309
Db 301 QDSLVCVTLA 309

RESULT 5
ADO29394
ID ADO29394 standard; protein; 309 AA.
XX ADO29394;
AC ADO29394;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR GPR35, SEQ ID NO:496.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
transgenic mouse; neurological disorder; adrenal gland disorder;
colon disorder; intestinal disorder; cardiovascular disorder;
muscular disorder; blood disorder; immune disorder; bone disorder;
joint disorder; metabolic disorder; nutritive disorder; cancer;
kidney disorder; liver disorder; lung disorder; breast disorder;
ovary disorder; uterus disorder; prostate disorder; testis disorder;
skin disorder; stomach disorder; pancreas disorder; spleen disorder;
thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
virucide; hepatotropic; antibacterial; antianaemic; antiseborrheic;
dermatological; antiulcer; antithyroid; antiallergic; anorectic;
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassiliatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO29916.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 496; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for

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CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 309 AA;
Query Match 100.0%; Score 1614; DB 8; Length 309;
Best Local Similarity 100.0%; Pred. No. 2.7e-167;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQWTETRIYMT 60
Db 1 MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQWTETRIYMT 60
QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
Db 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRH 120
QY 121 PLRAGLSRQAAAVCAVLVWLVIGSLVARWLLGQGGFCFSTRFNSMRPFLG 180
Db 121 PLRAGLSRQAAAVCAVLVWLVIGSLVARWLLGQGGFCFSTRFNSMRPFLG 180
QY 181 YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAARMWVANLLVFVVCFLPLHGLTVR 240
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRKAAARMWVANLLVFVVCFLPLHGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAKHS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYWAKEFOEASALAVAPRAKAKHS 300
QY 301 QDSLVCVTLA 309
Db 301 QDSLVCVTLA 309

RESULT 6
ADO78094
ID ADO78094 standard; protein; 309 AA.
XX ADO78094;
XX ADO78094;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human GPR35.
XX
KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;
KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;
KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;
KW melanoma; tumour; human; GPR35.
XX

```

OS Homo sapiens.  
 PN DE10254601-A1.  
 XX 03-JUN-2004.  
 XX 22-NOV-2002; 2002DE-01054601.  
 XX 22-NOV-2002; 2002DE-01054601.  
 XX (GANY-) GANYMED PHARM AG.  
 PA Tuereci O, Sahin U, Koslowski M;  
 PI WPI; 2004-421820/40.  
 DR N-PSDB; ADO78086.  
 XX Composition containing inhibitor of expression or activity of specific  
 PT tumor-associated antigens, useful for treating cancers, also related  
 PT compositions for diagnosis and monitoring.  
 XX Claim 72; SEQ ID NO 9; 124pp; German.  
 PS The invention relates to pharmaceutical compositions that comprise an  
 XX agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (Tag) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of Tag, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
 CC or cervix, also melanoma. Compositions containing Tag, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the amino acid  
 CC sequence of a human GPR35.  
 XX  
 SQ Sequence 309 AA;  
 Query Match 100.0%; Score 1614; DB 8; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIKLGFGYALGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFGYALGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120  
 QY 121 PLRAGLRSPQAAAVCAVWLVLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180  
 DB 121 PLRAGLRSPQAAAVCAVWLVLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180  
 QY 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYYWAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYYWAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVLA 309  
 DB 301 QDSLCTVLA 309  
 RESULT 7  
 ID ABG95172  
 XX ABG95172 standard; protein; 309 AA.  
 AC ABG95172;  
 XX 04-DEC-2002 (first entry)  
 XX

DE Human GPCR GPR35 mutant A216K.  
 XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
 KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
 KW psychotonic disorder; asthma; bronchospasm; anaesthesia;  
 KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
 KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 XX prostatic hypertrophy; receptor; mutant; mutin.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200268600-A2.  
 XX 06-SEP-2002.  
 XX 26-FEB-2002; 2002WO-US005625.  
 XX 26-FEB-2001; 2001US-0271913P.  
 XX (AREN-) ARENA PHARM INC.  
 XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX WPI; 2002-706980/76.  
 DR N-PSDB; ABS73401.  
 XX New human G-protein coupled receptor (GPCR), useful for screening agonist.  
 PT or inverse agonist compounds for treating diseases associated with GPCR.  
 XX Example 2; Page 189-190; 201pp; English.  
 XX The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
 CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents a mutant human GPCR  
 XX  
 SQ Sequence 309 AA;  
 Query Match 99.7%; Score 1609; DB 5; Length 309;  
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIKLGFGYALGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFGYALGVLLVGLLNSLALWVFCRMOQWTEIRYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTIAVDYVAVRH 120  
 QY 121 PLRAGLRSPQAAAVCAVWLVLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180  
 DB 121 PLRAGLRSPQAAAVCAVWLVLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLG 180  
 QY 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYYWAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYYWAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVLA 309  
 DB 301 QDSLCTVLA 309

```

Db      301 QDSLVCVTLA 309
RESULT 8
ID      AAY69989 standard; protein; 309 AA.
XX      AC      AAY69989;
XX      DT      31-MAY-2000 (first entry)
XX      DE      Human receptor-associated protein from Incyte clone 3083742.
XX      KW      Human receptor-associated protein; HRAP; Incyte clone 3083742;
KW      cystostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic;
KW      antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW      antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW      neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW      cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW      gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW      arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW      multiple sclerosis; irritable bowel syndrome.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
FT      Modified-site 2 /note= "Potential N-glycosylation site"
FT      Modified-site 79 /note= "Potential phosphorylation site"
FT      Modified-site 98 /note= "Potential phosphorylation site"
FT      Region 102..118
FT      /label= Signature_sequence
FT      /note= "G-protein coupled receptor"
FT      Modified-site 129 /note= "Potential phosphorylation site"
FT      Modified-site 165 /note= "Potential phosphorylation site"
FT      Modified-site 191 /note= "Potential phosphorylation site"
FT      Modified-site 212 /note= "Potential phosphorylation site"
FT      Modified-site 238 /note= "Potential phosphorylation site"
FT      Modified-site 253 /note= "Potential phosphorylation site"
FT      Modified-site 261 /note= "Potential phosphorylation site"
FT      /note= "Potential phosphorylation site"
XX      WO200008155-A2.
XX
XX      PD      17-FEB-2000.
XX
XX      PF      06-AUG-1999; 99WO-US017777.
XX
XX      PR      07-AUG-1998; 98US-0160065P.
XX      PR      01-SEP-1998; 98US-0098703P.
XX
XX      (INCY-) INCYTE PHARM INC.
XX
XX      PI      Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
XX      PI      Corley NC, Baughn MR;
XX
XX      DR      WPI; 2000-205710/18.
XX      DR      N-PSDB; AA250891.
XX
XX      PT      New human receptor-associated proteins (HRAP) useful for the diagnosis,
XX      PT      treatment and prevention of cell proliferative, autoimmune, inflammatory,
XX      PT      reproductive, cardiovascular, and gastrointestinal disorders.
XX
XX      PS      Claim 1; Page 76; 99pp; English.
XX

```

The present sequence is human receptor-associated protein (HRAP) from Incyte clone 3083742 obtained from OVARTUN01 cDNA library. This sequence is expressed in haematopoietic/immune, gastrointestinal and reproductive tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic, antiarthritic, antiasthmatic, osteopathic, antiallergic, antianaemic, antidiabetic, dermatological and neuroprotective activities. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with HRAP expression, especially cell proliferative, autoimmune/inflammatory, reproductive, cardiovascular and gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)

Query Match 99.6%; Score 1608; DB 3; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1.2e-166;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPPRAIKLGFYAYLGVLLVGLLNSLALWVFCRQQQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPPPRAIKLGFYAYLGVLLVGLLNSLALWVFCRQQQTETRIYMT 60

QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTATAVDRYVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTATAVDRYVAVRH 120

QY 121 PLRARGLSRPRQAAAVCAVLWLVIGLSVLRWLLGIQGGFCFRSTRNFMSPPLGLGF 180  
DB 121 PLRARGLSRPRQAAAVCAVLWLVIGLSVLRWLLGIQGGFCFRSTRNFMSPPLGLGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKARVMWANLLYFVVCFLPLHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKARVMWANLLYFVVCFLPLHVGLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYWMAKEFOEASALAVAPRAKAHS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYWMAKEFOEASALAVAPRAKAHS 300

QY 301 QDSLVCVTLA 309  
DB 301 QDSLVCVTLA 309

RESULT 9  
ADF70461  
ID ADF70461 standard; protein; 547 AA.  
XX AC ADF70461;  
XX DT 12-FEB-2004 (first entry)  
XX DE Orphan receptor ligand-related human protein SeqID84.  
XX KW ligand; orphan receptor protein; fusion protein; fluorescent protein;  
XX KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;  
XX KW GFPuv; Enhanced GFP; EGFP; human.  
XX OS Homo sapiens.  
XX PN WO2003071272-A1.  
XX PD 28-AUG-2003.  
XX PF 21-FEB-2003; 2003WO-JP001901.  
XX PR 22-FEB-2002; 2002JP-00045728.  
XX PR 23-JUL-2002; 2002JP-00213949.  
XX PR 11-OCT-2002; 2002JP-00298237.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX

PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
XX WPI; 2003-697654/66.  
XX N-PSDB; ADF70563.

XX Transformation of cells with a fusion protein of an orphan receptor  
XX protein with a fluorescent protein useful for identification of ligands  
XX to the orphan receptor.

XX Disclosure; SEQ ID NO 84; 594pp; Japanese.

XX This invention relates to a novel method of identifying ligands to an  
XX orphan receptor protein which comprises transforming cells with DNA  
XX encoding a fusion protein of the orphan receptor with a fluorescent  
XX protein, so that the fusion protein is expressed in the cells (or cell  
XX membranes isolated from them) and contacting the cells with the potential  
XX ligand to be tested. A suitable fluorescent protein for incorporation in  
XX the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
XX wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
XX identification of ligands binding to an orphan receptor protein.

XX Sequence 547 AA;

Query Match 99.6%; Score 1608; DB 7; Length 547;

Best Local Similarity 99.7%; Pred. No. 2.5e-166;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

Db 1 MNGTNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

QY 121 PLRARGLSRPRQAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180

Db 121 PLRARGLSRPRQAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKAAVMWVWVVCFLPLHVLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKAAVMWVWVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYWAKEFQASALAVAPRAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYWAKEFQASALAVAPRAKHS 300

QY 301 QDSLVCVTILA 309

Db 301 QDSLVCVTILA 309

RESULT 10

ADFS0511

ID ADFS0511 standard; protein; 309 AA.

XX ADFS0511;

XX ADFS0511;

DT 12-FEB-2004 (first entry)

XX Human GPCR GPR35 D113A mutein (SeqID 191).

DE mutant; mutein; transformation; endocrine cell line;

XX expression cloning system; bioactive peptide; GPCR ligand; human.

XX Synthetic.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

FT Misc-difference 113

XX /note= "wild type Asp substituted by Ala"

XX WO2003087366-A1.

XX 23-OCT-2003.

XX 16-APR-2003; 2003WO-JP004840.

XX 16-APR-2002; 2002JP-00113030.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;

XX Nishi T, Obinata M;

XX WPI; 2003-833737/77.

XX Endocrine cell lines originated from mammalian hypothalamus and

XX pancreatic islet, applicable in expression cloning systems of bioactive

XX peptide precursor genes, and in screening G protein-coupled receptor

XX ligands.

XX Example 24; SEQ ID NO 191; 316pp; Japanese.

XX This invention relates to a novel method for obtaining a DNA that encodes

XX a peptide acting as agonist, antagonist or inverse agonist on a target

XX receptor. Specifically, it comprises transformation of endocrine cell

XX lines originating from mammalian hypothalamus and pancreatic islets,

XX culturing the transformants and contacting with cells expressing the

XX target receptor. The identification of those cells with a response

XX reaction can be used for selecting a transformant cell line with the

XX appropriate target activity that is expressing the novel transformed DNA.

XX Accordingly, the present invention describes novel cell lines that are

XX applicable in expression cloning systems of bioactive peptide precursor

XX genes, and in screening GPCR ligands for use as drugs including agonists,

XX antagonists and inverse agonists i.e. activators and inhibitors. Such

XX cell lines can provide a highly sensitive and convenient GPCR ligand

XX assay system. This polypeptide sequence is the human GPCR GPR35 D113A

XX mutein of the invention.

XX Sequence 309 AA;

Query Match 99.5%; Score 1606; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 2e-166;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

Db 1 MNGTNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

Db 61 NLAVADLCCLCTLPFVLSLRDTSPTPLCSQGIYLTNRYSISLVTIAVDYVAVRH 120

QY 121 PLRARGLSRPRQAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180

Db 121 PLRARGLSRPRQAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKAAVMWVWVVCFLPLHVLTVR 240

Db 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKAAVMWVWVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYWAKEFQASALAVAPRAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYWAKEFQASALAVAPRAKHS 300

QY 301 QDSLVCVTILA 309

Db 301 QDSLVCVTILA 309

RESULT 11

AAVS8645

ID AAVS8645 standard; protein; 309 AA.

XX AAVS8645;

XX AAVS8645;

XX 11-APR-2000 (first entry)

XX Human G-protein coupled receptor GPR35A.

XX GPR35A; human; G-protein coupled receptor; purinergic;  
 KW 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;  
 KW cytostatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;  
 KW hypotensive; hypertensive; osteopathic; antianginal; cardiant;  
 KW cerebroprotective; antiulcer; antiallergic; antimagraine; antiemetic;  
 KW tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;  
 KW therapy; diagnosis; vaccine.

XX Homo sapiens.

XX ADA84069

XX WO9964452-A1.

XX 16-DEC-1999.

XX 01-JUN-1999; 99WO-US012123.

XX 11-JUN-1998; 98US-00096031.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Elshourbagy NA;

XX WPI; 2000-116525/10.

XX N-PSDB; AA235390.

XX New human GPR35A polypeptides and polynucleotides used to identify  
 PT agonists, antagonists and inhibitors for use in therapy.

XX Claim 1; Page 32-33; 38pp; English.

XX The present sequence represents human GPR35A, a novel member of the  
 CC purinergic family of polypeptides and a G-protein coupled receptor. The  
 CC invention provides GPR35A polypeptides having at least 70% identity with  
 CC the present sequence, GPR35A polynucleotides, recombinant materials, and  
 CC methods for their production. GPR35A polypeptides can be used for  
 CC identifying agonists and antagonists/inhibitors, and for detecting  
 CC diseases associated with inappropriate GPR35A activity or levels. GPR35A  
 CC polypeptides and polynucleotides, agonists, antagonists and antibodies  
 CC are used to treat: infections such as bacterial, fungal, protozoan and  
 CC viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;  
 CC obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart  
 CC failure; hypotension; hypertension; urinary retention; osteoporosis;  
 CC angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign  
 CC prostatic hypertrophy; migraine; vomiting; psychotic and neurological  
 CC disorders including anxiety, schizophrenia, manic depression, depression,  
 CC delirium, dementia and severe mental retardation; and dyskinesias such as  
 CC Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also  
 CC useful for production of vaccines

XX Sequence 309 AA;

Query Match 99.3%; Score 1602; DB 3; Length 309;  
 Best Local Similarity 99.4%; Pred. No. 5.4e-166;  
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPPAIKGYPAYLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
 |||||||  
 DB 1 MNGTYNTCGSSDLTPPAIKGYPAYLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60  
 |||||||

QY 61 NLAVALDCLLCTLPFVHLSDRTSDTFLCQLSQGIYLTNRYSISLTAIAVDYVAVRH 120  
 |||||||

DB 61 NLAVALDCLLCTLPFVHLSDRTSDTFLCQLSQGIYLTNRYSISLTAIAVDYVAVRH 120  
 |||||||

QY 121 PLRARGLRPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTRHFNFSRPFLLGF 180  
 |||||||

DB 121 PLRARGLRPRQAAVCAVLWLVIGSLVARWLLGQEGGFCFRSTRHFNFSRPFLLGF 180  
 |||||||

QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAAARMVWVANLLVFVVCFLPLHVLTVR 240  
 |||||||

DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAAARMVWVANLLVFVVCFLPLHVLTVR 240  
 |||||||

QY 241 LAVGNACALLETIRRALYITTSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKHS 300  
 |||||||

DB 241 LAVGNACALLETIRRALYITTSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKHS 300  
 |||||||

QY 301 QDSLCLCVTLA 309  
 |||||||

DB 301 QDSLCLCVTLA 309  
 |||||||

RESULT 12

ADA84069

ID ADA84069 standard; protein; 309 AA.

XX AC ADA84069;

XX 20-NOV-2003 (first entry)

XX Human GPR35 protein.

XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;  
 KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;  
 KW vaccine.

XX Homo sapiens.

XX WO2002103028-A2.

XX 27-DEC-2002.

XX 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.

PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.

XX (BIOM-) BIOMEDICAL CENT.

PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;  
 WPI; 2003-175241/17.

DR N-PSDB; ADA84068.

XX Determining if a nucleic acid is a marker for a phenotype/cell type of  
 PT interest, by global comparison of expressed sequence tags known to be  
 PT expressed in the phenotype/cell type with all ESTs expressed in normal  
 PT tissue.

XX Claim 29; Page 448-449; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid  
 CC is a marker for a predetermined phenotype/cell type of interest from a  
 CC biological species. The method comprises performing a global comparison  
 CC of a group of expressed sequence tags (ESTs) known to be expressed in the  
 CC phenotype/cell type of interest with all ESTs expressed in normal tissue  
 CC in order to identify ESTs that are preferentially expressed in the  
 CC phenotype/cell of interest. A method of the invention is useful for  
 CC determining whether a nucleic acid is a marker for a predetermined  
 CC phenotype or cell type of interest from a biological species, preferably  
 CC Arabidopsis or human. The cell type of interest is an abnormal cell such  
 CC as a tumour cell, and the predetermined phenotype is a stress-induced  
 CC phenotype such as hyperosmotic stress or high salt conditions. A method  
 CC of the invention is also useful for determining the progression of colon  
 CC cancer in a human, for detecting a tumour cell, and for regulating or  
 CC preventing the growth of a tumour cell. An antibody of the invention is  
 CC useful for detecting the absence or presence of peptides encoded by  
 CC tumour-associated markers. A polypeptide of the invention is useful as an  
 CC immunogen for vaccinating an animal. The present sequence represents a  
 CC tumour-associated antigen of the invention.

XX Sequence 309 AA;



Query Match 99.3%; Score 1602; DB 6; Length 309;  
Best Local Similarity 99.4%; Pred. No. 5.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60  
DB 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120  
DB 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120

QY 121 PLRAGLSRPRQAAAVCAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180  
DB 121 PLRAGLSRPRQAAAVCAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180

QY 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAAVMWVANLLVVFVCFPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAAVMWVANLLVVFVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITTSKLSNDANCCLDACIYYIMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETIRRALYITTSKLSNDANCCLDACIYYIMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLCTVTLA 309  
DB 301 QDSLCTVTLA 309

RESULT 13  
AD078095  
ID AD078095 standard; protein; 394 AA.  
XX AC AD078095;  
XX DT 26-AUG-2004 (first entry)  
XX DE Human GPR35 isoform.  
XX KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
XX KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
XX KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
XX KW melanoma; tumour; human; GPR35.  
XX OS Homo sapiens.  
XX PN DE10254601-A1.  
XX PD 03-JUN-2004.  
XX PF 22-NOV-2002; 2002DE-01054601.  
XX PR 22-NOV-2002; 2002DE-01054601.  
XX PA (GANY-) GANYMED PHARM AG.  
XX PI Tuereci O, Sahin U, Koslowski M;  
XX XX  
XX WPI; 2004-421820/40.  
XX  
XX Composition containing inhibitor of expression or activity of specific  
XX tumor-associated antigens, useful for treating cancers, also related  
XX compositions for diagnosis and monitoring.  
XX  
XX Claim 72; SEQ ID NO 10; 124pp; German.  
XX  
XX The invention relates to pharmaceutical compositions that comprise an  
XX agent that inhibits the expression or activity of a tumour-associated  
XX antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX compositions and related compositions, are used for treatment of diseases  
XX associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney

CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
CC acid, antibodies or host cells, are also useful for diagnosis and  
CC monitoring of tumours. The present sequence represents the amino acid  
CC sequence of a human GPR35.  
XX  
SQ Sequence 394 AA;

Query Match 99.3%; Score 1602; DB 8; Length 394;  
Best Local Similarity 99.4%; Pred. No. 7.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPFAIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60  
DB 86 MNGTYNTCGSSDLTWPFAIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 145

QY 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 120  
DB 146 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIAVDVRYAVRH 205

QY 121 PLRAGLSRPRQAAAVCAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180  
DB 206 PLRAGLSRPRQAAAVCAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 265

QY 181 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAAVMWVANLLVVFVCFPLPHVGLTVR 240  
DB 266 YLPLAVVVFCSLKVVYVTAQAORPPTDVGOAEATRKAAVMWVANLLVVFVCFPLPHVGLTVR 325

QY 241 LAVGNACALLETIRRALYITTSKLSNDANCCLDACIYYIMAKEFOEASALAVAPRAKAHKS 300  
DB 326 LAVGNACALLETIRRALYITTSKLSNDANCCLDACIYYIMAKEFOEASALAVAPRAKAHKS 385

QY 301 QDSLCTVTLA 309  
DB 386 QDSLCTVTLA 394

RESULT 14  
ADRI0454  
ID ADRI0454 standard; protein; 394 AA.  
XX AC ADRI0454;  
XX DT 04-NOV-2004 (first entry)  
XX DE Human protein useful for treating neurological disease Seq 3960.  
XX KW human; oligo-capping method; diagnostic marker; Gene therapy;  
XX KW osteoporosis; neurological disease; Alzheimer's disease;  
XX KW Parkinson's disease; dementia; short memory; cancer;  
XX KW sense or motor function; emotional reaction; fear response; panic;  
XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
XX KW tranquiliser.  
XX OS Homo sapiens.  
XX PN EP1447413-A2.  
XX PD 18-AUG-2004.  
XX PF 12-FEB-2004; 2004EP-00003145.  
XX PR 14-FEB-2003; 2003JP-00102207.  
XX PR 09-MAY-2003; 2003JP-00131452.  
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
XX PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX WPI; 2004-583265/57.  
XX DR N-PSDB; ADRI0415.  
XX  
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
PS  
XX Claim 1; SEQ ID NO 3960; 2686pp; English.

CC This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteoprotective, neuroprotective, neurotropic, antiparkinsonian,  
CC cytotactic and tranquiliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
CC office.  
XX  
SQ Sequence 394 AA;

Query Match 99.3%; Score 1602; DB 8; Length 394;  
Best Local Similarity 99.4%; Pred. No. 7.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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DB 266 YLPLAVVFCSLKVVTALAQRPPTDVGQAEATRKARMYWANLLVFVVCFLPLHGLTVR 325  
  
QY 241 LAVGNACALLETIRALYITSKLSDANCCLDIAICYYYMAKEFOEASALAVAPRAKAHS 300  
DB 326 LAVGNACALLEMIRALYITSKLSDANCCLDIAICYYYMAKEFOEASALAVAPRAKAHS 385  
  
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AC ADP29765;  
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DT 12-AUG-2004 (first entry)  
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DE Human secreted protein SEQ ID #532.  
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KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.  
PF 29-AUG-2002; 2002US-0406576P.  
XX 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
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PR 18-APR-2003; 2003US-0463700P.  
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PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
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PR 08-AUG-2003; 2003US-0493341P.  
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XX  
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
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XX  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS  
PS Claim 1; SEQ ID NO 1763; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
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Best Local Similarity 99.6%; Pred. No. 5.2e-142;  
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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QY 241 LAVGNACALLETIRRALYITSKLSD 266  
Db |||||||  
241 LAVGNACALLETIRRALYITSKLSD 266

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
1879.324 Million cell updates/sec

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1614	100.0	309	9	US-09-768-877-20
2	1614	100.0	309	14	US-10-225-567A-492
3	1614	100.0	309	17	US-10-696-639-44
4	1602	99.3	309	14	US-10-157-031-351
5	402	24.9	370	10	US-09-964-821B-11
6	402	24.9	370	14	US-10-081-810-44
7	402	24.9	370	14	US-10-225-567A-225
8	402	24.9	370	14	US-10-024-298A-176
9	402	24.9	370	14	US-10-042-211A-176
10	402	24.9	370	14	US-10-268-332-11
11	402	24.9	370	15	US-10-617-217A-176
12	402	24.9	370	17	US-10-753-267-86
13	401	24.8	370	10	US-09-964-821B-10

14	401	24.8	370	14	US-10-268-332-10	Sequence 10, Appl
15	392	24.3	370	14	US-10-024-298A-174	Sequence 174, App
16	392	24.3	370	14	US-10-042-211A-174	Sequence 174, App
17	392	24.3	370	15	US-10-617-217A-174	Sequence 174, App
18	381.5	23.6	363	16	US-10-314-048A-159	Sequence 159, App
19	381.5	23.6	363	16	US-10-897-815-159	Sequence 159, App
20	376.5	23.3	363	10	US-09-930-334-16	Sequence 16, Appl
21	376.5	23.3	363	15	US-10-619-141-16	Sequence 16, Appl
22	376	23.3	319	14	US-10-167-192-1	Sequence 1, Appl
23	376	23.3	319	15	US-10-400-991-4	Sequence 4, Appl
24	375.5	23.3	363	14	US-10-321-807-36	Sequence 36, Appl
25	375.5	23.3	363	15	US-10-295-027-226	Sequence 226, App
26	375.5	23.3	363	15	US-10-292-798-668	Sequence 668, App
27	375.5	23.3	363	16	US-10-321-807-36	Sequence 36, Appl
28	375.5	23.3	363	16	US-10-314-048A-36	Sequence 36, Appl
29	375.5	23.3	363	16	US-10-897-815-36	Sequence 36, Appl
30	375.5	23.3	364	14	US-10-017-161-766	Sequence 766, App
31	375.5	23.3	392	14	US-10-017-161-808	Sequence 808, App
32	371.5	23.0	387	10	US-09-930-334-2	Sequence 2, Appl
33	371.5	23.0	387	15	US-10-619-141-2	Sequence 2, Appl
34	368.5	22.8	308	10	US-09-991-225-7	Sequence 7, Appl
35	368.5	22.8	308	10	US-09-964-821B-12	Sequence 12, Appl
36	368.5	22.8	308	14	US-10-268-332-12	Sequence 12, Appl
37	368.5	22.8	308	15	US-10-369-405-7	Sequence 7, Appl
38	368.5	22.8	339	14	US-10-188-149A-4	Sequence 4, Appl
39	368.5	22.8	387	9	US-09-944-807-21	Sequence 21, Appl
40	368.5	22.8	387	14	US-10-092-135-8	Sequence 8, Appl
41	368.5	22.8	387	14	US-10-251-385-108	Sequence 108, App
42	368.5	22.8	387	14	US-10-251-385-222	Sequence 222, App
43	368.5	22.8	387	14	US-10-240-842-4	Sequence 4, Appl
44	368.5	22.8	387	14	US-10-225-567A-281	Sequence 281, App
45	368.5	22.8	387	14	US-10-296-223-4	Sequence 4, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/768,877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422,869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-768-877-20

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DB 1 MNGYNTCGSSDLTPWPAIKLGFYALGVLLVLGLLNSLALWVFCRCMQWTTETRIYMT 60

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RESULT 2
US-10-225-567A-492
; Sequence 492, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Rough, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 492
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-492

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US-10-696-639-44
; Sequence 44, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 309
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-696-639-44

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Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-10-157-031-351
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; Publication No. US20030108990A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 351
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
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DB 121 PLRARGLRPQAAVAVLWLVGSLVAVRWLGIQEGGCFRSTRHNFNSMRPPLG 180

QY 181 YLPLAVVVFCSLKVVYALQRPPTDVQAEATRKAAWVWVNLVVFVCFPLHVLTVR 240  
DB 181 YLPLAVVVFCSLKVVYALQRPPTDVQAEATRKAAWVWVNLVVFVCFPLHVLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCDLDAICYYYMAKEFOASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCDLDAICYYYMAKEFOASALAVAPRAKAHKS 300

QY 301 QDSLCTVLA 309  
DB 301 QDSLCTVLA 309

## RESULT 5

US-09-964-821B-11  
; Sequence 11, Application US/09964821B  
; Publication No. US20030186360A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M. G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBEMV3,  
; FILE REFERENCE: D0042NP  
; CURRENT APPLICATION NUMBER: US/09/964,821B  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,783  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-821B-11

Query Match 24.9%; Score 402; DB 10; Length 370;  
Best Local Similarity 34.1%; Pred. No. 6.3e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVLSVFCRMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRHPLRARGLSPROQAAVCAVL 140  
DB 104 WPFQGT-LCKISGTAFLTNIGSMFLFCTCISVDRLAIVYVPSRTIRTRNSAIVCAGV 162

## RESULT 7

QY 141 WVLVIGSLVARWLLGIQIE-----GGFCFRSTRHNFNSMR--FPLLGFVLPLAVVVF 189  
DB 163 WILVSGGISASLFTSTNNVNNATTTCFEGFSKRVMKTYLSKITIFIEVVGFIIPLNLVS 222

QY 190 CSLKVVTALAQRPTDVQAEAT-RKAARMWVWVNLVVFVCFPLHVLTVRLAVGWNAC 248  
DB 223 CSSVVLRTL--RKPAATLSQIGTNKKVLMITVHMAVVFVCPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANCCDLDAICYYYMAKEFOASALAVAPRAKAHKSQDSL 305  
DB 281 TNCFLERPAKIMYPITLCLATLNCDFPIYVFTLESFQKSPYI-----NAHIRMESLP 334

QY 306 VT 307  
DB 335 KT 336

RESULT 6  
US-10-081-810-44  
; Sequence 44, Application US/10081810  
; Publication No. US20030064438A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI-  
; FILE REFERENCE: D0132 NP  
; CURRENT APPLICATION NUMBER: US/10/081,810  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: US 60/270,793  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/270,792  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/296,427  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-081-810-44

Query Match 24.9%; Score 402; DB 14; Length 370;  
Best Local Similarity 34.1%; Pred. No. 6.3e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVGLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLITNSVLSVFCRMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQLSQGIYLTNRYSISLVTAIAVDVAVRHPLRARGLSPROQAAVCAVL 140  
DB 104 WPFQGT-LCKISGTAFLTNIGSMFLFCTCISVDRLAIVYVPSRTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIQIE-----GGFCFRSTRHNFNSMR--FPLLGFVLPLAVVVF 189  
DB 163 WILVSGGISASLFTSTNNVNNATTTCFEGFSKRVMKTYLSKITIFIEVVGFIIPLNLVS 222

QY 190 CSLKVVTALAQRPTDVQAEAT-RKAARMWVWVNLVVFVCFPLHVLTVRLAVGWNAC 248  
DB 223 CSSVVLRTL--RKPAATLSQIGTNKKVLMITVHMAVVFVCPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANCCDLDAICYYYMAKEFOASALAVAPRAKAHKSQDSL 305  
DB 281 TNCFLERPAKIMYPITLCLATLNCDFPIYVFTLESFQKSPYI-----NAHIRMESLP 334

QY 306 VT 307  
DB 335 KT 336

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US-10-225-567A-225
; Sequence 225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLVGLLVGLLLNSLALWFCRMOQWETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY      82  -DTSPTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGLRSPROAAVCAVL 140
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
104  WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIYVPRSTIRTRNSAIVCAGV 162

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKWKYLSKITIFIEVVGFIPLILNVS 222

QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWANLLVFVFCPLPLHVLGTVRLAVGWNA 248
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
223  CSSVVLRTL--RKPAATLSQIGTNKKVKLMITVHMAVFVVCVFPVNSVLFYALVRSQAI 280

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSLC 305
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334

QY      306  VT 307
Db      |
335  KT 336

RESULT 8
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24

US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLVGLLVGLLLNSLALWFCRMOQWETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY      82  -DTSPTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGLRSPROAAVCAVL 140
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
104  WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIYVPRSTIRTRNSAIVCAGV 162

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKWKYLSKITIFIEVVGFIPLILNVS 222

QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWANLLVFVFCPLPLHVLGTVRLAVGWNA 248
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
223  CSSVVLRTL--RKPAATLSQIGTNKKVKLMITVHMAVFVVCVFPVNSVLFYALVRSQAI 280

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSLC 305
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334

QY      306  VT 307
Db      |
335  KT 336
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```
US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLVGLLVGLLLNSLALWFCRMOQWETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY      82  -DTSPTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGLRSPROAAVCAVL 140
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
104  WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIYVPRSTIRTRNSAIVCAGV 162

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKWKYLSKITIFIEVVGFIPLILNVS 222

QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWANLLVFVFCPLPLHVLGTVRLAVGWNA 248
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
223  CSSVVLRTL--RKPAATLSQIGTNKKVKLMITVHMAVFVVCVFPVNSVLFYALVRSQAI 280

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSLC 305
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334

QY      306  VT 307
Db      |
335  KT 336

RESULT 9
US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLVGLLVGLLLNSLALWFCRMOQWETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY      82  -DTSPTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGLRSPROAAVCAVL 140
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
104  WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIYVPRSTIRTRNSAIVCAGV 162

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKWKYLSKITIFIEVVGFIPLILNVS 222

QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWANLLVFVFCPLPLHVLGTVRLAVGWNA 248
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
223  CSSVVLRTL--RKPAATLSQIGTNKKVKLMITVHMAVFVVCVFPVNSVLFYALVRSQAI 280

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKSQDSLC 305
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334

QY      306  VT 307
Db      |
335  KT 336
```



```
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRCMQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIGQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMTVHMAVFCVFPYNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERFAKIMYPITLCATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESL 334
QY 306 VT 307
DB 335 KT 336
RESULT 10
US-10-268-332-11
; Sequence 11, Application US/10268332
; Publication No. US2003017548A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHLY
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-11
Query Match 24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRCMQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIGQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNAC 248
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRCMQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIGQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNAC 248
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DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMTVHMAVFCVFPYNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERFAKIMYPITLCATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESL 334
QY 306 VT 307
DB 335 KT 336
RESULT 11
US-10-617-217A-176
; Sequence 176, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-kB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176
Query Match 24.9%; Score 402; DB 15; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRCMQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVLSVLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPLRAGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIGQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMTVHMAVFCVFPYNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYYMAKEFOEASALAVAPRAKAHKSODSLC 305
DB 281 TNCFLERFAKIMYPITLCATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESL 334
QY 306 VT 307
DB 335 KT 336
RESULT 12
US-10-753-267-86
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Publication No. US20030175748A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY3, EXPRESSED HIGHLY
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY3, EXPRESSED HIGHLY
FILE REFERENCE: D0042A CIP
CURRENT APPLICATION NUMBER: US/10/268,332
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: U.S. 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: U.S. 60/261,783
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: U.S. 60/305,085
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: U.S. 60/313,171
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: U.S. 09/964,821
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 370
TYPE: PRT
ORGANISM: Homo sapiens
US-10-268-332-10

Query Match      24.8%; Score 401; DB 14; Length 370;
Best Local Similarity 34.0%; Pred. No. 7.9e-30;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

Qy      25 AYLGVLVGLGLLSLALWVFCRMOQWTEIRYMTNLAVADLCLLCTLPF-VLHSLR-- 81
Db      44 AVYSVVFILGILITNSASLWVFCRMRSETATFITNLAVSDLLFVCTLPFKIFYNFRH 103
Qy      82 -DTSPTLQSLQSGIYLTNRYSISLVTAIAVDYVAVRHPLRAGLSRQAAAVCAVL 140
Db      104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIVYFPRSTIRTRNSAIVCAGV 162
Qy      141 WVLVIGSIVARWLLGIQEGF-----CFR-----STRHNFNSMRFPPLLGFL 182
Db      163 WILVLSG-----GISASLSTNNVNTTCFEGLSKRVKTYLSKITIFIEVVGFI 215
Qy      183 PLVVVFCSLKVVTALAQRPTDVQAEAT-RKAARMVWMLLVFVVCFLPLHVLGLTVRL 241
Db      216 PLILNVSCSVVLRTL--RKPATLSQIGTNKKVKLMTVHMAVVFVCFVPYNSVLFLYA 273
Qy      242 AVGNWAC--ALLETRRALLY-ITSKLSDANCLDAICYVMKAEQASALAVAPRAK 298
Db      274 LVRQAITNCFERFAKIMYRITLCLATLNCDFDPFIYFTLESFQKSYI-----NAH 327
Qy      299 KSQDSLCTV 307
Db      328 IRMESLFT 336

RESULT 15
US-10-024-298A-174
Sequence 174, Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
APPLICANT: AKIO MATSUDA
APPLICANT: GOICHI HONDA
APPLICANT: SHUJI MURAMATSU
APPLICANT: YUKIKO NAGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR FILING DATE: 2001-03-26
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; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP008912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-298A-174

Query Match      24.3%; Score 392; DB 14; Length 370;
Best Local Similarity 34.5%; Pred. No. 5.7e-29;
Matches 97; Conservative 58; Mismatches 104; Indels 22; Gaps 9;

Qy      25 AYLGVLVGLGLLSLALWVFCRMOQWTEIRYMTNLAVADLCLLCTLPF-VLHSLR-- 81
Db      44 AVYSVVFILGILITNSASLWVFCRMRSETATFITNLALSDLLFVCTLPFKIFYNFRH 103
Qy      82 -DTSPTLQSLQSGIYLTNRYSISLVTAIAVDYVAVRHPLRAGLSRQAAAVCAVL 140
Db      104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRFLAIVYFPRSTIRTRNSAIVCAGV 162
Qy      141 WVLVIGSIVARWLLGIQEGF-----GGFCFRSTRHNFNSMR--FPLLGFLVPLAVVVF 189
Db      163 WILVLSGGLSASLSTNNVNTTCFEGFSKRVKTYLSKITIFIEVVGFIPLILNV 222
Qy      190 CSLKVVTALAQRPTDVQAEAT-RKAARMVWMLLVFVVCFLPLHVLGLTVRLAVGNWAC 248
Db      223 CSSVVLRTL--RKPATLSQIGTNKKVKLMTVHMAVVFVCFVPYNSVLFYALVRSQAI 280
Qy      249 --ALLETRRALLY-ITSKLSDANCLDAICYVMKAEQEA 286
Db      281 TNCLLERFAKIMYRITLCLATLNCDFDPFIYFTLESFQKS 321

Search completed: May 23, 2005, 11:33:02
Job time : 56 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 11:09:25 ; Search time 58.5 Seconds  
(without alignments)  
2704.829 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKHSQDSLCTVLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1603	99.3	309	1 GP35 HUMAN	Q9hc97 homo sapien
2	1597	98.9	394	2 Q6ZMP9	Q6zmp9 homo sapien
3	1123	69.5	307	1 GP35 MOUSE	Q9es90 mus musculus
4	1122	69.5	307	2 Q8CB97	Q8cb97 mus musculus
5	1108	68.6	307	2 Q8BS98	Q8bs98 mus musculus
6	401	24.8	370	1 P2Y9 HUMAN	Q99677 homo sapien
7	399	24.7	370	2 Q6NSP5	Q6nsp5 homo sapien
8	399	24.7	370	2 Q8BKK1	Q8bkk1 mus musculus
9	391	24.2	370	2 Q8BLG2	Q8blg2 mus musculus
10	376.5	23.3	363	2 Q8TDS4	Q8tds4 homo sapien
11	374	23.2	319	2 Q8N580	Q8n580 homo sapien
12	369.5	22.9	387	1 G09B HUMAN	P49019 homo sapien
13	369.5	22.9	387	2 Q8NGE4	Q8nge4 homo sapien
14	367.5	22.8	308	1 P2Y5 CHICK	P32250 gallus gall
15	366	22.7	347	2 Q7ZSA4	Q7zsa4 brachydanio
16	360.5	22.3	296	2 Q9WU09	Q9wu09 rattus norv
17	360.5	22.3	344	1 P2Y5 HUMAN	P43657 homo sapien
18	360.5	22.3	344	2 Q7Z3S0	Q7z3s0 homo sapien
19	360.5	22.3	344	2 Q7Z3S6	Q7z3s6 homo sapien
20	360	22.3	372	1 GP32 HUMAN	Q9hlc0 homo sapien
21	356.5	22.1	344	1 P2Y5 MOUSE	Q8bmc0 mus musculus
22	348.5	21.6	360	2 Q9EP66	Q9ep66 mus musculus
23	338	20.9	319	2 Q9Y2T6	Q9y2t6 homo sapien
24	337.5	20.9	360	2 Q80Z39	Q80z39 rattus norv
25	330	20.4	298	2 Q8VE54	Q8ve54 mus musculus
26	329.5	20.4	374	1 P2Y2 RAT	P41232 rattus norv
27	328.5	20.3	377	1 P2Y2 HUMAN	P41231 homo sapien
28	326	20.2	346	1 GP81 HUMAN	Q9bxc0 homo sapien
29	321.5	19.9	345	1 CLT2_PIG	Q95n03 sus scrofa
30	320	19.8	349	2 Q6P852	Q6p852 xenopus tro
31	319.5	19.8	343	1 GP81 MOUSE	Q8c131 mus musculus

32	319.5	19.8	361	1 P2Y4 RAT	O35811 rattus norv
33	319	19.8	346	2 Q6NXU5	Q6nxu5 homo sapien
34	317	19.6	373	1 P2Y2 MOUSE	P35383 mus musculus
35	316.5	19.6	346	1 CLT2 HUMAN	Q9ns75 homo sapien
36	316	19.6	309	1 CLT2 RAT	Q924t9 rattus norv
37	316	19.6	362	1 P2YR_CHICK	P34996 gallus gall
38	316	19.6	362	1 P2YR_MELGA	P49652 meleagris g
39	316	19.6	374	2 O57466	O57466 meleagris g
40	315.5	19.5	365	1 P2Y4 HUMAN	P51582 homo sapien
41	314.5	19.5	361	1 P2Y4 MOUSE	Q91js7 mus musculus
42	314.5	19.5	398	1 BRB2 RAT	P25023 rattus norv
43	314	19.4	328	1 P2Y6 RAT	Q63371 rattus norv
44	311.5	19.3	362	1 GP84 HUMAN	P46093 homo sapien
45	311.5	19.3	362	2 Q6NWM4	Q6nwm4 homo sapien

#### ALIGNMENTS

#### RESULT 1

GP35\_HUMAN  
ID GP35\_HUMAN STANDARD; PRT; 309 AA.  
AC Q9HC97; O43495; Q86UH4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Probable G protein-coupled receptor GPR35.  
GN Name=GPR35;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;  
RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,  
RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;  
RT "Discovery of three novel G-protein-coupled receptor genes."  
RL Genomics 47:310-313(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;  
RP MET-253 AND SER-294.  
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,  
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
RA Bell G.I.;  
RT "Genetic variation in the gene encoding calpain-10 is associated with  
type 2 diabetes mellitus."  
RL Nat. Genet. 26:163-175(2000).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT SER-294.  
RA Warren C.N., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues  
examined, including pancreatic islets and skeletal muscle, with  
relatively higher levels in adult lung, small intestine, colon and  
stomach.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC ----- AF027957; AAC52028.1; -
DR EMBL; AF089087; AAG17965.1; -
DR EMBL; AY275467; AAP32299.1; -
DR EMBL; HGNC:4492; GPR35.
DR MIM; 602646; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
DR KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT DOMAIN 1 24 Extracellular (Potential).
FT TRANSMEM 25 45 1 (Potential).
FT DOMAIN 46 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 90 Extracellular (Potential).
FT TRANSMEM 91 112 3 (Potential).
FT DOMAIN 113 135 Cytoplasmic (Potential).
FT TRANSMEM 136 156 4 (Potential).
FT DOMAIN 157 174 Extracellular (Potential).
FT TRANSMEM 175 195 5 (Potential).
FT DOMAIN 196 218 Cytoplasmic (Potential).
FT TRANSMEM 219 239 6 (Potential).
FT DOMAIN 240 258 Extracellular (Potential).
FT TRANSMEM 259 279 7 (Potential).
FT DOMAIN 280 309 Cytoplasmic (Potential).
FT DISULFID 89 162 By similarity.
FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
FT VARIANT 25 25 A -> T.
FT VARIANT 29 29 /FTID=VAR_013601.
FT VARIANT 108 108 /FTID=VAR_013602.
FT VARIANT 125 125 /FTID=VAR_013603.
FT VARIANT 125 125 /FTID=VAR_013604.
FT VARIANT 253 253 /FTID=VAR_013605.
FT VARIANT 294 294 /FTID=VAR_013606.
FT CONFLICT 174 174 A -> R (in Ref. 1).
FT SEQUENCE 309 AA; 34141 MW; FC034FB7231B26F1 CRC64;

Query Match 99.3%; Score 1603; DB 1; Length 309;
Best Local Similarity 99.4%; Pred. No. 8.3e-112;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60
Db 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60
QY 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIADRYVAVRH 120
Db 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIADRYVAVRH 120
QY 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
Db 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
QY 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
Db 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
QY 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWVWVNLVFPVVCFLPLHVLGTVR 240
Db 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWVWVNLVFPVVCFLPLHVLGTVR 240
QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDACIYYNMAKEFQESALAVAPRAKAHKS 300
Db 241 LAVGNACALLETTIRRALYITSKLSDANCCLDACIYYNMAKEFQESALAVAPRAKAHKS 300
QY 301 QDSCVLTLA 309
Db 301 QDSCVLTLA 309
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RESULT 2
Q6ZMP9
ID Q6ZMP9 PRELIMINARY; PRT; 394 AA.
AC Q6ZMP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16773.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK131540; BAD18676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
DR KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 394 AA; 43308 MW; 1598FD4BAE4233C CRC64;

Query Match 98.9%; Score 1597; DB 2; Length 394;
Best Local Similarity 99.0%; Pred. No. 2.8e-111;
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60
Db 86 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 145
QY 61 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIADRYVAVRH 120
Db 146 NLAVADLCLLCTLPFVLHSLRDTSDTPLCQLSQGIYLTNRYMSISLVTAIADRYVAVRH 205
QY 121 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 180
Db 206 PLRARGLRSPROAAAVCAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLIGF 265
QY 181 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWVWVNLVFPVVCFLPLHVLGTVR 240
Db 266 YLPLAVVFCSLKVVTALAQRPPTDVGOAEATRKARVMWVWVNLVFPVVCFLPLHVLGTVR 325
QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDACIYYNMAKEFQESALAVAPRAKAHKS 300
Db 326 LAVGNACALLETTIRRALYITSKLSDANCCLDACIYYNMAKEFQESALAVAPRAKAHKS 385
QY 301 QDSCVLTLA 309
Db 386 QDSCVLTLA 394

RESULT 3
GP35_MOUSE
ID GP35_MOUSE STANDARD; PRT; 307 AA.
AC Q9ES90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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DE Probable G protein-coupled receptor GPR35.  
GN Name=Gpr35;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RX SEQUENCE FROM N.A.  
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
RA Hinokio Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,  
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
RA Bell G.I.;  
RT "Genetic variation in the gene encoding calpain-10 is associated with  
RT type 2 diabetes mellitus.";  
RL Nat. Genet. 26:163-175(2000).  
RN [2];  
RP SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF200349; AAB18487.1; -;  
DR EMBL; BC027429; AAG27429.1; -;  
DR MGD; MGI:1929509; Gpr35.  
DR InterPro; IPR000276; GPCR Rhodopsn.  
DR InterPro; IPR002286; P2\_purnocptor.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1\_1; 1.  
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
FT DOMAIN 1 18 Extracellular (Potential).  
FT TRANSMEM 19 39 1 (Potential).  
FT DOMAIN 40 53 Cytoplasmic (Potential).  
FT TRANSMEM 54 74 2 (Potential).  
FT DOMAIN 75 88 Extracellular (Potential).  
FT TRANSMEM 89 110 3 (Potential).  
FT DOMAIN 111 129 Cytoplasmic (Potential).  
FT TRANSMEM 130 150 4 (Potential).  
FT DOMAIN 151 176 Extracellular (Potential).

FT TRANSMEM 177 197 5 (Potential).  
FT DOMAIN 198 217 Cytoplasmic (Potential).  
FT TRANSMEM 218 238 6 (Potential).  
FT DOMAIN 239 257 Extracellular (Potential).  
FT TRANSMEM 258 278 7 (Potential).  
FT DOMAIN 279 307 Cytoplasmic (Potential).  
FT DISULFID 87 160 By similarity.  
FT CARBOHYD 2 2 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 7 7 N-linked (GlcNAc... ) (Potential).  
SQ SEQUENCE 307 AA; 34151 MW; 0B3D02CECB16710D CRC64;  
Query Match 69.5%; Score 1123; DB 1; Length 307;  
Best Local Similarity 71.9%; Pred. No. 5.3e-76;  
Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;  
QY 1 MNGTYNTCGSSDLTWPPAIGVAYLGVLLVGLLLNSLALWVFCRCMQQTETRIYMT 60  
DB 1 MNST--TCNST-LTWPAVNNFFIYSALLLVGLLLNSVALWVFCYRHHQWETRIYMT 57  
QY 61 NLAVADLCLLCTLPVLSLR-DTSDFLCQLSQIYITNRYMSISLVTAIADVAVR 119  
DB 58 NLAVADLCLLCSLPVLSYSLKYSSTDFVCSQIYILANRYMSISLVTAIADVAVR 117  
QY 120 HPLRARGLRSPQAAAVCAVLWLVIGSIVARWLLGIOGGFCFRS-TRHNFSNMFPL 178  
DB 118 HPLRARELRSPQAAAVCALWVIVVTSLVWRRLGMOEGGFCFSQTRNFSSTAFSL 177  
QY 179 GFYPLAVVVFCSLVVTTALAQRPPTDVQAEATKAKRMVWVANLVFVVCFLPLHVL 238  
DB 178 GFYPLAVVVFCSLVVTTALSRPAADVQAEATKATHWVANLVFVVCFLPLHVL 237  
QY 239 VRLAVGNWACALLETIRALVITSKLSANCLDAICYYYMAKPFQEQASALAVAPRAH 298  
DB 238 VQVSLNLTCAARDTFSRALSITGKLSDTNCLDAICYYYMAKPFQEQASALAVAPRAH 296  
QY 299 KSQSLCVTL 308  
DB 297 KSQSLCVTL 306  
RESULT 4  
QSCB97 PRELIMINARY; PRT; 307 AA.  
ID Q8CB97  
AC Q8CB97  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Mus musculus adult male bone cDNA, RIKEN full-length enriched library,  
DE clone:9830121M19 product:G protein-coupled receptor 35, full insert  
DE sequence.  
GN Name=Gpr35;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RX SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-5;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2];  
RP SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3];  
RP SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Bone;  
RA The FANTOM Consortium,





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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK034870; BAC28861.1; -.
DR MGD; MGI:1929509; Gpr35.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_puroceptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01157; P2PURNOCPTR.
DR PROSITE; PS00237; G-PROTEIN RECF1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF1_2; 1.
DR PROSITE; PS0262; G-PROTEIN RECF1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;
Query Match 68.6%; Score 1108; DB 2; Length 307;
Best Local Similarity 71.3%; Pred. No. 6.9e-75;
Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;
Qy 1 MNGVTNCGSDLTWPPAIIKLGFAVLGVLLVGLLLNSLWVFCRCMQWTERIYMT 60
Db 1 MNST--TCNST-LTPASVNNFFIYISALLLVGLLLNSLWVFCYRMHWTERIYMT 57
Qy 61 NLAVADLCLCTLPVLSLRLS- DTS DTPCLCOLSQGIYLTNRYSLSLTATADVRYAVR 119
Db 58 NLAVADLCLCLSPVLSLKYSSSDTPVCQLSQGIYLANRYSLSLTATADVRYAVR 117
Qy 120 HPLRARGLRSPQAAAVCAVLVVLVIGSLVAVRLVGLIQQGFCFRS- TRHNFNSMRPFL 178
Db 118 HPLRARELRSPQAAAVCAVLVVLVTVSLVVRWRLGMOEGGFCFSQTRRNPSTTAFSLL 177
Qy 179 GFYLPVAVVFCSLKVVVTAQAQRPDVGQAEATKAKRWYWANLLVFWVCFPLHVLGT 238
Db 178 GFYLPVAVVFCSLQVTVLGRPPADVGQAEATKATHMWYWANLVAVFVCFPLHVLVT 237
Qy 239 VRLVAVGNACALLEITIRALYITTSKLSDANCCLDALCYVYMAKEFQEASALAVAPRAKH 298
Db 238 VQVSLNLTCAARDTFSRALSTITKLSDTNCCLDALCYVYMAKEFQEAFAKPTSNT-PH 296
Qy 299 KQSDSLCVTL 308
Db 297 KQYSQILSL 306
RESULT 6
ID P2Y9 HUMAN STANDARD; PRT; 370 AA.
AC Q99677; O15132;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE P2Y purinoceptor 9 (p2Y9) (Purinegenic receptor 9) (G protein-coupled

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DE receptor GPR23) (P2Y5-like receptor).
GN Name=GPR23; Synonym=P2RY9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97225799; PubMed=9073069; DOI=10.1016/S0378-1119(96)00722-6;
RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,
RT Kolakowski L.F. Jr., Lynch K.R., George S.R.;
RT "Cloning and chromosomal mapping of four putative novel human G-
RT protein-coupled receptor genes.";
RL Gene 187:75-81(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97366605; PubMed=9223435; DOI=10.1006/dbrc.1997.6895;
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;
RT "Cloning of a human heptahelical receptor closely related to the P2Y5
RT receptor.";
RL Biochem. Biophys. Res. Commun. 236:106-112(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,
CC putamen, caudate, frontal cortex, pons, hypothalamus and
CC hippocampus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC
DR EMBL; U66578; AAC51301.1; -.
DR EMBL; U90323; AAB62087.1; -.
DR EMBL; U90322; AAB62088.1; -.
DR EMBL; AF005419; AAB65322.1; -.
DR EMBL; AY301274; AAP58404.1; -.
DR EMBL; AL590083; CAD18851.1; -.
DR PIR; JC5549; JCS549.
DR HSSP; P34996; 1DDD.
DR Genew; HGNC:4478; GPR23.
DR MIM; 300086; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR002188; P2Y5_puroceptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECF1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 43 Extracellular (Potential).
FT TRANSMEM 44 64 1 (Potential).
FT DOMAIN 65 73 Cytoplasmic (Potential).
FT TRANSMEM 74 94 2 (Potential).

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FT DOMAIN          95 112 Extracellular (Potential).
FT TRANSMEM       113 133 3 (Potential).
FT TRANSMEM       134 155 Cytoplasmic (Potential).
FT TRANSMEM       156 176 4 (Potential).
FT TRANSMEM       177 203 Extracellular (Potential).
FT TRANSMEM       204 224 5 (Potential).
FT TRANSMEM       225 254 Cytoplasmic (Potential).
FT TRANSMEM       255 275 6 (Potential).
FT TRANSMEM       276 294 Extracellular (Potential).
FT TRANSMEM       295 315 7 (Potential).
FT TRANSMEM       316 370 Cytoplasmic (Potential).
FT DISULFID       111 188 By similarity.
FT CARBOHYD       15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       183 183 N-linked (GlcNAc...) (Potential).
FT CONFLICT       192 192 F -> L (in Ref. 3).
SQ SEQUENCE       370 AA; 41895 MW; 20857F52A3929E48 CRC64;

Query Match          24.8%; Score 401; DB 1; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.5e-22;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVLLVGLLNSLALWVFCRQMQWTEIRYMTNLAVALDCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPKFIYFNHRH 103

QY 82 -DTSPTPLCOLSQGIIYLTNRYSISLVTAIAVDYVAVRHPLRAGLRSPQAAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLTNIYGSMLFLTCISVDRELAIVYPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222

QY 190 CSLKVVVTAALORPPTDVQAEAT-RKAKRWVWVNLVVFVCFPLPLHVLGTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVLMITVHMVAVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCDAICYYIMAKFQEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERFAKIMYPITLCLATLNCDFDPFIYFTLESFQKSPYI-----NAHIRMESL 334

QY 306 VT 307
DB 335 KT 336

RESULT 7
Q6NSP5 PRELIMINARY; PRT; 370 AA.
AC Q6NSP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor 23.
GN Name=GPR23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069996; AAH69996.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-..; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin..; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR002188; P2Y5_purinocptor.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PRINTS; PR01067; P2Y5ORPHANR.
DR PROSITE; PS0237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 370 AA; 41867 MW; 2AB4B3F5F43FF83 CRC64;

Query Match          24.7%; Score 399; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-22;
Matches 103; Conservative 59; Mismatches 112; Indels 28; Gaps 10;

QY 25 AYLVLLVGLLNSLALWVFCRQMQWTEIRYMTNLAVALDCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPKFIYFNHRH 103

QY 82 -DTSPTPLCOLSQGIIYLTNRYSISLVTAIAVDYVAVRHPLRAGLRSPQAAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLTNIYGSMLFLTCISVDRELAIVYPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTCFEGFSKRVKMTYLSKITIFIEVVGFIPIILNVS 222

QY 190 CSLKVVVTAALORPPTDVQAEAT-RKAKRWVWVNLVVFVCFPLPLHVLGTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVLMITVHMVAVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCDAICYYIMAKFQEASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERFAKIMYPITLCLATLNCDFDPFIYFTLESFQKSPYI-----NAHIRMESL 334

QY 306 VT 307
DB 335 KT 336

RESULT 8
Q6BKK1 PRELIMINARY; PRT; 370 AA.
AC Q6BKK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE 'enriched library, clone:DI30067B12 product:P2Y PURINOCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;

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OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=24099374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitzunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa E., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK051709; BAC34729.1; --  
 DR MGD; MGI:1925384; Gpr23.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045028; P:purinergic nucleotide receptor activity; IEA.  
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR InterPro; IPR002188; P2Y5\_purinocptor.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PRINTS; PR01067; P2Y5ORPHAN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1\_1; UNKNOWN 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1\_2; 1.  
 SQ SEQUENCE 370 AA; 41956 MW; ABI26B42343AS6E1 CRC64;  
 Query Match 24.7%; Score 399; DB 2; Length 370;  
 Best Local Similarity 34.3%; Pred. No. 6.3e-22;  
 Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;  
 QY 4 TVNTGSSDLTPPPAIGLGFY-AYLGVLVLLGLINSLALWVFCRMOQWTEIRYMTNL 62  
 DB 27 TNNICIVDD-----SFKNLNGAVSVVFLGLITNSASLFFCFRMMKRSATFIYNL 81  
 QY 63 AVADLCCLCTLPF-VLHSLR---DTSDFPLCOLSQGIYLTNRYMSISLVTAIVDRYVAV 118  
 DB 82 ALSDLLFVCTLPFKIFYFNHRHWPFGDT-LCKISGTAFLTIYSGMLFLTCISVDRFLAI 140  
 QY 119 RHPLRARGLRSPQAAAYCAVLWLVIGSLVARWLLGIQE-----GGCFRSTRHN 169  
 DB 141 VYPPRSRTIRTRNSAIVCAGWILVNGGISASLFTTNVNNATTTTCFEGFSKRWKTY 200  
 QY 170 FNSMR--FPLLGFLPLAVVFCVSLKVVTAALAQRPPTDVGQAEAT-RKAKRMVWNLVLF 226  
 DB 201 LSKITIFIEVVGFIILPLINVCSSVLURTL--RKPAILSQLGTNKKVKVLMITVMAVF 258  
 QY 227 VVCFPLHVLGTVRLAVGNAC--ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEF 283  
 DB 259 VVCFVPYNSVLFYALVRSQAITNCLLRFPAKIMYPITLCLATLNCDFPFIYYFLESF 318  
 QY 284 QEA 286  
 DB 319 QKS 321  
 RESULT 9  
 Q8BLG2 PRELIMINARY; PRT; 370 AA.  
 ID Q8BLG2  
 AC Q8BLG2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length  
 DE enriched library, clone:BI30055L15 product:P2Y PURINOCEPTOR 9, full  
 DE insert sequence.  
 GN Name=Gpr23;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RT Genome Res. 10:1757-1771(2000).
RL [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akai H., Tanaka T., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK045289; BAC32299.1; -.
DR MGD; MG1:1925384; Gpr23.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002188; P2Y5_purinocptor.
DR Pfam; PF00001; 7tm1.1; -.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
SQ SEQUENCE 370 AA; 41872 MW; 0E4C79FEDFD32050 CRC64;
Query Match 24.2%; Score 391; DB 2; Length 370;
Best Local Similarity 34.5%; Pred. No. 2.5e-21;
Matches 97; Conservative 59; Mismatches 103; Indels 22; Gaps 9;
QY 25 AVYGVLLVGLLLNSLALWVFCRCMQQWTEIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
Db 44 AVYVVFILGLITSSASLAFVFCRMRKMSRTAIFITNLALSLLFVCTLPFFIFYNR 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRGLRSPROAAAVCAVL 140
Db 104 WFGGDT-LCKISGTAFPLTNIYSGMLFLTCISVDRLAIVIPRSTRIRRNLSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIGQE-----GGFCFRSTRHFNFSMR--FPLLGFLPLAVVVF 189
Db 163 WILVLSGGISASLFSFTNNVNTTTCFEGFSKRVKWTYLSKITIFIEVVGFIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVGQAEAT-RKAKRMWANLLVFFVFCPLHVLGTLVLAAGWAC 248
Db 223 CSSVVLRTL--RKPATLSIGTNKKKVLKMTVHMAVFFVVCVFPVNSVFLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSDANCCLDAICYYMAKEFOEA 286
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Db 281 TNCLLERFAKIMYPITLCLATLNCFCDFPFYIYFTLESQKS 321
RESULT 10
Q8TDS4 PRELIMINARY; PRT; 363 AA.
AC Q8TDS4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor HM74a (Seven transmembrane helix
DE receptor).
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elehourbacy N.,
RA Elliott M., Ignar D.M., Murock P.R., Stepkowski K., Green A.,
RA Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA Wilson S., Pike N.B.;
RT "Molecular identification of high and low affinity receptors for
RT nicotinic acid.";
RL J. Biol. Chem. 278:9869-9874(2003).
RN [3]
RP SEQUENCE FROM N.A.
RA Elehourbacy N.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB083632; BAB93345.1; -.
DR EMBL; AY148884; AAN71621.1; -.
DR EMBL; AB065876; BAC06094.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01157; P2YEURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41849 MW; C4B0EBC9CCB81D56 CRC64;
Query Match 23.3%; Score 376.5; DB 2; Length 363;
Best Local Similarity 34.8%; Pred. No. 3e-20;
Matches 97; Conservative 45; Mismatches 104; Indels 33; Gaps 11;
QY 27 LGVLIVLGLLLNSLALWVFCRCMQQWTEIYMTNLAVALDCLLCTLPFVLHSL-----R 81
Db 34 LGLEIFIFGLLGLALWIFCFHLKSKSRIFLFLNLAVADFLIICLPFLMDNYVRRWDW 93
QY 82 DTSPTPLCOLSQGIYLTNRYSISLVTAIVDRYVAVRHPLRGLRSPROAAAVCAVLW 141
Db 94 KFGDIP-CRLMLFMLAMNRQSGIIFLTVAVDYRFRVVRVPHALNKISNRTAAISCLLW 152
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QY 142 VLVIGSLV--ARWLLGIEGG--FCFR-STRHNF--NMRPPLIGFYPLAVVFCSLKV 194  
 Db 153 GITTGLTAVHLLKKWPIQGGANLCSFSICHTFQHEAMF--LLEFFFLGIIILFCSARI 211  
 QY 195 VTLAQRPTDVGQAEATKAKR---MYWANLVFVVCFLPLHVLGLTVRLAVGM----- 245  
 Db 212 IWSLQR-----QMDRAKIKRAITFMVAIVEVICFLP---SVVRIIFWLLHTSG 262  
 QY 246 -NACALLETIRRALYITKLSANDCLDAICYYNMAKEF 283  
 Db 263 TQNCVEVRSVDLAFITILSFTYMSMLDPVVYFSSPSF 301

RESULT 11  
 QBN580  
 ID QBN580 PRELIMINARY; PRT; 319 AA.  
 AC QBN580;  
 DT 01-OCT-2002 (Tremblrel. 22, Created)  
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE G protein-coupled receptor 55 (GPR55 protein) (Fragment).  
 GN Name=GPR55;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Roha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
 RA Korn B., Zuo D., Hu Y., Labaer J.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; BC032694; AAH32694.1; -;  
 DR EMBL; CR541776; CAG46575.1; -;  
 DR Genew; HGNC:4511; GPR55.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 319 AA; 36637 MW; D6E5C6CA8426E7D5 CRC64;

Query Match 23.2%; Score 374; DB 2; Length 319;  
 Best Local Similarity 35.5%; Pred. No. 4.1e-20;  
 Matches 98; Conservative 49; Mismatches 95; Indels 34; Gaps 10;

QY 32 VLGLLSLALWVFC-----RMQQTETRIYMTNLAVADLCILCTLPFLVLSLRDTSPT 87  
 Db 32 VLGLLLNLLAHTGFTFLKRWPDYAATSIYMINLAVFDLLVLSPFKVLSQVQSPFP 91  
 QY 88 -LCQLSQGIYLTNRYMSISLVATAVDYVAVRPLRGLRSPROAAVCAVLWLV-I 145  
 Db 92 SLCTLVECLYFVSMYGSVFTTCISMDRFLAIRYPLLVSRLSPRKIFGICCTIWLVT 151  
 QY 146 GSLVARMLLGIEGGFCFRSTRHNF-----SMRFPL--LGFLYPLAVVFCSLKVTA 197  
 Db 152 GSIRIYSPHGVKVKMCF-----HNMSSDWTSAKVFPPLEVFGLLPMGIMFGCCRSIHI 207  
 QY 198 LAQRPTDVGQAEATR---KAKRWV---ANLLVFVVCFLPLHVLGLTVRLAVGMW---AC 248  
 Db 208 L-----LGRDHTQDWVQKACIYIAASLAVFVVSFLPVHLGFFLQFLVRNSFIVEC 260  
 QY 249 ALLETIRRALYITKLSANDCLDAICYYNMAKEFQ 284  
 Db 261 RAKQISFFLQLSMCFSNVNCCLDFVCYFVKEFR 296

RESULT 12  
 G09B HUMAN  
 ID G09B HUMAN STANDARD; PRT; 387 AA.  
 AC P49019;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Probable G protein-coupled receptor GPR109B (G protein-coupled  
 DE receptor HM74).  
 GN Name=GPR109B; Synonyms=HM74;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RA MEDLINE=94092629; PubMed=7505609;  
 RA Nomura H., Nielsen B.W., Matsushima K.;  
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative  
 RT leukocyte chemotactic peptide receptors";  
 RL Int. Immunol. 5:1239-1249 (1993).  
 CC -!- FUNCTION: Orphan receptor.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D10923; BAA01721.1; -;  
 DR F01; I69202; I69202.  
 DR HSSP; P34996; 1DDD.  
 DR Genew; HGNC:16824; GPR109B.  
 DR MIM; 606039; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.

GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.

DR InterPro; IPR002286; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1.1;  
DR PRINTS; PR00237; GPCR\_HODOPSIN.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1\_1;  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2\_1;  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 387 AA; 44495 MW; 26433C855E85EC81 CRC64;

Query Match 22.9%; Score 369.5; DB 2; Length 387;  
Best Local Similarity 34.8%; Pred. No. le-19;  
Matches 97; Conservative 44; Mismatches 105; Indels 33; Gaps 11;

QY 27 LGVLLVLGLLNSLALWFCRCMQQTETRIYMTNLAVADLCILCTLPFVLHSLRDTSDT 86  
DB 34 LGLEFIPLGLNGLALWIFCFHLKSWKSRIFLFNLAADVADFLIICLPFFVNDYYRRSDW 93

QY 87 PL-----COLSQGIYLTNRYSISLVTAIVDVRVAVRHRLARGLSRPRQAACAVLW 142  
DB 94 KFGDIPCRLLVFMFAMNRQSGIIFLTVAVDVRYFRVVPHHALNKISNTAAIISCILLWG 153

QY 143 LVIG---SLVARWLIGIQEG--GFCFR-STRNHF--NSMRPPLLGFYLPLAVVVFCSLKV 194  
DB 154 ITVGLTVHLKKLL-IQGNPANVCISFSICHTFRWEAMP-LLEFLLPLGLILFCSARI 211

QY 195 VTALAQRPTDVGAERAKR---MVWANLVVVCFLPHVGLTVRLAVGW-----245  
DB 212 IWSLRQ-----QMDRAIKRAITFMVVAIVFVICFLP---SVVVRIRIFMLLHTSG 262

QY 246 -NACALLETRRALYTISKLSDNCCCLDAICYYYMAKEF 283  
DB 263 TQNCVEYRSVDLAFFITLSFTYMNSMLDPPVYFSSPSF 301

RESULT 14  
ID QNGE4 PRELIMINARY; PRT; 308 AA.  
AC QNGE4 STANDARD; PRT; 308 AA.

DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).  
GN Name=P2Y5;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]\_TaxID=9031;  
RP SEQUENCE FROM N.A.  
RC TISSUE=T-cell;  
RX MEDLINE=93329058; PubMed=8939036;  
RA Kaplan M.H., Smith D.I., Sundick R.S.;  
RT "Identification of a G protein coupled receptor induced in activated T cells."  
RL J. Immunol. 151:628-636(1993).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Induced in activated T-cells.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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EMBL; L06109; AB06597.1; -.  
PIR; I50241; I50241.  
DR HSP; P34996; 1DDP.



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